

# STIC Search Report Biotech-Chem Library

#### STIC Database Tracking Number: 118756

TO: Michael Borin-

Location: rem/2a55/2c70

**Art Unit: 1631** 

Tuesday, April 06, 2004

Case Serial Number: 09/997807

From: Edward Hart

**Location: Biotech-Chem Library** 

**REM-1A55** 

Phone: 571-272-2512

edward.hart@uspto.gov

#### Search Notes

Examiner Borin,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

**Edward Hart** 



Pending Nucleic Acid and Pending Amino Acid database searches generate two sets of results each. The Pending databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Searches run against the Nucleic Acid Pending database produce two sets of results, with the extensions .rnpm and .rnpn

Searches run against the Amino Acid Pending database produce two sets of results, with the extensions .rapm and .rapn

Because they contain data that is confidential, the results of Pending database searches should not be left in the case.

#### STIC-Biotech/ChemLib

From:

Borin, Michael

Sent:

Monday, April 05, 2004 6:04 PM

To: Subject: STIC-Biotech/ChemLib Search request:09/997807

Examiner: M.Borin

AU: 1631

Remsen 2A55 Tel.: 20713

RE: 09/997807; peptide polymer

Please conduct search of polypeptide SEQ ID No. 2 against the commercial and interference protein databases.

Thank you

Searcher:\_ Phone: Location: Date Picked Up: 4/16 Date Completed: Searcher Prep/Review Clerical: Online time:

TYPE OF SEARCH:	
NA Sequences:	
AA Sequences:	
Structures:	
Bibliographic:	
Litigation:	
Full text:	
Patent Family:	
Other:	

VENDOR/COST (where applic.) STN:\_ DIALOG: Questel/Orbit:\_ DRLink:\_ Lexis/Nexis: Sequence Sys.: www/Internet: Other (specify):\_



#### STIC SEARCH RESUL FEEDBACK FORM

#### Biotech-Chem Library

Questions about the scope or the results of the search? Contact the searcher or contact:

Mary Hale, Information Branch Supervisor 571-272-2507 Remsen E01 D86

0	luntary Results Feedback Form
۶	I am an examiner in Workgroup: Example: 1610
خ	Relevant prior art found, search results used as follows:
	☐ 102 rejection
	103 rejection
	Cited as being of interest.
	Helped examiner better understand the invention.
	Helped examiner better understand the state of the art in their technology.
	Types of relevant prior art found:
	Foreign Patent(s)
	Non-Patent Literature  (journal articles, conference proceedings, new product announcements etc.)
خ	Relevant prior art <b>not found:</b>
	Results verified the lack of relevant prior art (helped determine patentability).
	Results were not useful in determining patentability or understanding the invention
on	nments:

Drop off or send completed forms to STIC/Biotech-Chem Library Remsen Bldg.



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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model - protein search, protein

(without alignments) 974.789 Million cell updates/sec April 6, 2004, 12:24:31; Search time 60 Seconds Run on:

1 VKYTTLAIAGIIASAAALAL......EGMLFDSLPVIFNFQVLQVG 207 US-09-997-807-2 Title: Perfect score: Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

1586107 Total number of hits satisfying chosen parameters:

1586107 seqs, 282547505 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp1980s:\*
geneseqp1990s:\*
geneseqp2000s:\*
geneseqp2001s:\* geneseqp2002s:\* geneseqp2003as:\* A\_Geneseq\_29Jan04:\* geneseqp2003bs:\* geneseqp2004s:\* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Description	Aau99735 Pyrodicti	Adb46044 CanA fusi		Adb46046 CanB fusi	Aau99737 Pyrodicti	Adb46048 Canc fusi	Aau99739 Pyrodicti	Adb46052 CanE fusi	Aau99738 Pyrodicti	Adb46050 CanD fusi	Ade45056 CAMP fact	Abu33304 Protein e	Abp30785 Streptoco		Abb57211 Mouse isc	Aay77286 Streptomy		Aau82974 S. cerevi	Abr53317 Protein s	Abp65732 Bifidobac	Abb93924 Herbicida	Aaw98010 BCG Ag85B	Abu08321 M. bovis	Abp65592 Bifidobac	Aau84295 Human end
ID	AAU99735	ADB46044	AAU99736	ADB46046	AAU99737	ADB46048	AAU99739	ADB46052	AAU99738	ADB46050	ADE45056	ABU33304	ABP30785	ADC51492	ABB57211	AAY77286	AAY78838	AAU82974	ABR53317	ABP65732	ABB93924	AAW98010	ABU08321	ABP65592	AAU84295
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ABB90742	ABU54449	ABP27517	AAG51600	AAG06413	AAG51599	AAG06412	AAE36342	ABU24247	AAW43448	ABB47321	ABB47302	ABP73966	ABU50834	ABU51217	AAR05710	AAR06478	AAR43675	AAR99645
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833	9 9 9 9	83	82.5	82.5	82.5	82.5	82,5	82.5	81.5	81.5	81.5	81	80.5	80.5	80.5	80.5	80.5	80.5
26	28	29	30	31	32	33	34	35	36	37	38	33	40	41	42	43	44	45

#### ALIGNMENTS

RESULT 1 AAU99735

AAU99735 standard; protein; 207 AA.

AAU99735;

(first entry) 07-OCT-2002

Pyrodictium abyssi Cannule A (CanA) protein.

Polymer; self-assembly; divalent cation; drug delivery; human body; animal body; fibre; polymeric separation agent; coating composition; biochip; nanomechanical component; optical switch; optical wave guide; cannule A; CanA.

Pyrodictium abyssi.

WO200244336-A2.

06-JUN-2002.

30-NOV-2001; 2001WO-US045001.

30-NOV-2000; 2000US-0250426P.

(DIVE-) DIVERSA CORP.

Chow K; Barton N, Lafferty WM, Short J, Mathur EJ,

WPI; 2002-557536/59. N-PSDB; ABK88271. 

Producing a polypeptide polymer by self-assembly for use in lubricants and coating compositions, comprises polymerizing polypeptides capable of self-assembly in the presence of a divalent cation and template molecule.

Claim 9; Page 178-179; 182pp; English.

The present invention relates to a new method of producing a polypeptide polymer by self-assembly. The method involves providing a number of polypeptides capable of self-assembly in the presence of a divalent cation and polymerising the polypeptides in the presence of a divalent cation and a template molecule. The invention is useful for delivering a drug to a location in the human or animal body. Polypeptides are useful for encapsulating a molecule. The polymeric separation agent is useful for isolating a chiral compound from a mixture. A nucleic acid is useful for comparing a first sequence to a second sequence, where the first sequence is a nucleic acid, and for identifying a feature in a particular

Sequence 207 AA;

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sequence. The polypeptide of the invention is useful in fibres, polymeric esparation agentes, coating compositions, biochips, nanomechanical components, optical switches and optical wave guides. The present amino acid sequence represents the Pyrodictium abyssi Cannule A (CanA) protein
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chimeric cannulae polypeptide; metabolite exchange; signal compound;
        ADB46044 standard; protein; 207 AA
                         (first entry)
                                 CanA fusion protein.
                                                     Pyrodictium abyssi.
                         04-DEC-2003
                ADB46044;
                                              CanA.
RESULT 2
ADB46044
ID ADB4
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18-FEB-2003; 2003WO-US004828. WO2003070961-A1. 28-AUG-2003.

(DIVE-) DIVERSA CORP.

15-FEB-2002; 2002US-0357406P.

O'donoghue 2003-689787/65. N-PSDB; ADB46043 Barton NR,

Frey G;

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New chimeric polypeptide comprising a first domain comprising a cannulae polypeptide and a second domain comprising a heterologous polypeptide or peptide useful for selecting and purifying chiral compositions from racemic mixtures,

Claim 3; Page 81-82; 89pp; English.

second domain having a heterologous polypeptide or peptide. The polypeptides, nanotubule and methods are useful for identifying, separating and synthesizing proteins or ligands, and for selecting and purifying chiral compositions from racemic mixtures. The nanotubule is useful for cells to exchange metabolites, genetic information or signal compounds. The present sequence represents CanA fusion protein. The present invention relates to a chimeric cannulae polypeptide

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                                                                                                                                                                                                                                       GAQGSDDIGYALVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNFS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polymer; self-assembly; divalent cation; drug delivery; human body; animal body; fibre; polymeric separation agent; coating composition; biochip; nanomechanical component; optical switch; optical wave guide; cannule B; CanB.
                                                                         1 VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAA
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                                      0;
   Length 207;
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100.0%; Score 1042; DB 7; 100.0%; Pred. No. 9.8e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                           AAU99736 standard; protein; 170 AA.
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                                  Matches 207;
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Sequence 170 AA;

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separation agents, coating compositions, bicchips, nanomechanical components, optical switches and optical wave guides. The present amino acid sequence represents the Pyrodictium abyssi Cannule B (CanB) protein
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                                                                                                                                                                  33; Indels
                                                                                                                           53.1%; Score 553.5; DB 5 60.2%; Pred. No. 1.7e-46; iive 12; Mismatches 33
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acid sequence
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ADB46046 standard; protein; 170 AA (first entry) CanB fusion protein. 04-DEC-2003 ADB46046; RESULT 4 ADB4604

chimeric cannulae polypeptide; metabolite exchange; signal compound; Pyrodictium abyssi. WO2003070961-AI. 28-AUG-2003 

15-FEB-2002; 2002US-0357406P. 18-FEB-2003; 2003WO-US004828

(DIVE-) DIVERSA CORP

O'donoghue E, WPI; 2003-689787/65. Barton NR,

Ö Frey

New chimeric polypeptide comprising a first domain comprising a cannulae polypeptide and a second domain comprising a heterologous polypeptide for peptide useful for selecting and purifying chiral compositions from racemic mixtures. N-PSDB; ADB46045.

Claim 3; Page 82-83; 89pp; English.

The present invention relates to a chimeric cannulae polypeptide and a second domain having a heterologous polypeptide or peptide. The polypeptides, nanotubule and methods are useful for identifying, separating and synthesizing proteins or ligands, and for selecting and purifying chiral compositions from racemic mixtures. The nanotubule is useful for cells to exchange metabolites, genetic information or signal compounds. The present sequence represents CanB fusion protein.

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                                                                                                                                      GAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNFS 120
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                                                                    1 VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAA 60
                                   37;
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53.1%; Score 553.5; DB 7 60.2%; Pred. No. 1.7e-46;
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Pyrodictium abyssi Cannule C (CanC) protein. AAU99737 standard; protein; 178 AA (first entry) 07-0CT-2002 AAU99737;

AAU9973 RESULT

animal body, fibre, polymeric separation agent; coating composition, biochip, nanomechanical component, optical switch; optical wave guide; Cannule C; CanC. self-assembly; divalent cation; drug delivery; human body; Polymer; 

Pyrodictium abyssi.

WO200244336-A2

06-JUN-2002

30-NOV-2001; 2001WO-US045001.

30-NOV-2000; 2000US-0250426P.

(DIVE-) DIVERSA CORP.

Chow K; Barton N, Lafferty WM, Short J, Mathur EJ,

WPI; 2002-557536/59. N-PSDB; ABK88273 Producing a polypeptide polymer by self-assembly for use in lubricants and coating compositions, comprises polymerizing polypeptides capable of self-assembly in the presence of a divalent cation and template molecule.

Claim 9; Page 180; 182pp; English.

polymer by self-assembly. The method involves providing a number of polymer by self-assembly. The method involves providing a number of cation and polymerising the polypeptides in the presence of a divalent cation and a template molecule. The invention is useful for delivering a for encapsulating a molecule. The invention is useful for delivering a for encapsulating a molecule. The polymeric separation agent is useful for isolating a chiral compound from a mixture. A nucleic acid is useful for isolating a first sequence to a second sequence, where the first sequence is a nucleic acid, and for identifying a feature in a particular sequence. The polypeptide of the invention is useful in fibres, polymeric separation agents, coating compositions, biochips, nanomechanical The present invention relates to a new method of producing a polypeptide

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onents, optical switches and optical wave guides. The present amino sequence represents the Pyrodictium abyssi Cannule C (CanC) protein
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                                                                                                                                                                                                                                                                     AGAĞGYKDMGYIKITNQSKVNVIKLKVTLANAEQLKPYFDYLQLVLTS----NATGT---
                                                                                                                                                                                                                                         1 VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHL-GSITPA
                                                                                                                                                                                              36; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chimeric cannulae polypeptide; metabolite exchange; signal compound;
                                                                                                                                                Length 178;
                                                                                                                                         51.8%; Score 540; DB 5; Length 178
58.5%; Pred. No. 3.9e-45;
ive 22; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180 FKAFYEAKEGMLFDSLPVIFNFOVL 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               146 VEÁYÝEÁKEGMLFDSLPVILNFOVL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADB46048 standard; protein; 178 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Frey G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DMVKAVLSLEKPSAVIILDNDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-FEB-2003; 2003WO-US004828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-FEB-2002; 2002US-0357406P
                                                                                                                            Query Match
Best Local Similarity 58.59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New chimeric polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barton NR, O'donoghue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CanC fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2003-689787/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pyrodictium abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADB46047.
                                                of the invention
                                                                                              Sequence 178 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003070961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-DEC-2003
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     components,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB46048;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 6
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The present invention relates to a chimeric cannulae polypeptide and a second domain having a heterologous polypeptide or peptide. The polypeptides, nanotubule and methods are useful for identifying, separating and synthesizing proteins or ligands, and for selecting putifying chiral compositions from racemic mixtures. The nanotubule is useful for cells to exchange metabolites, genetic information or signal compounds. The present sequence represents CanC fusion protein.

Sequence 178 AA;

Claim 3; Page 83-84; 89pp; English.

racemic mixtures.

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60 AGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNF 119
                                                                                                                                                                                                                                   120 SETKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVAILN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polymer by self-assembly. The method involves providing a number of polymer by self-assembly. The method involves providing a number of cation and bolymerising the polypeptides in the presence of a divalent cation and a template molecule. The invention is useful for delivering a drug to a location in the human or animal body. Polypeptides are useful for encapsulating a molecule. The polymeric separation agent is useful for isolating a chiral compound from a mixture. A nucleic acid is useful for comparing a first sequence to a second sequence, where the first sequence is a nucleic acid, and for identifying a feature in a particular sequence. The polypeptide of the invention is useful in fibres, polymeric separation agents, coating compositions, biochips, nanomechanical components, optical switches and optical wave guides. The present amino
                                                                                                                                                                                                                                                                        ------YDSTNKIO-LK 145
                                                                                    59
                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and coating compositions, comprises polymerizing polypeptides capable of self-assembly in the presence of a divalent cation and template molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present nvention relates to a new method of producing a polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polymer; self-assembly; divalent cation; drug delivery; human body; animal body; fibre; polymeric separation agent; coating composition; biochip; nanomechanical component; optical switch; optical wave guide;
                                                                                                      Producing a polypeptide polymer by self-assembly for use in lubricants
                                                                                                                                                                                             61 AGAQGYKDMGYIKITNQSKVNVIKLKVTLANAEQLKPYFDYLQLVLTS----NATGT---
                                                                                 1 VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHL-GSITPA
                                             Gaps
                                               36;
         Length 178;
       51.8%; Score 540; DB 7; Length 17
58.5%; Pred. No. 3.9e-45;
ive 22; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pyrodictium abyssi Cannule E (CanE) partial protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Barton N,
                                                                                                                                                                                                                                                                                                            204
                                                                                                                                                                                                                                                                                                                                           146 VEAYYEAKEGMLFDSLPVILNFQVL 170
                                                                                                                                                                                                                                                                                                            180 FKAFYEAKEGMLFDSLPVIFNFOVL
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAU99739 standard; protein; 124 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lafferty WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 182; 182pp; English,
                                                                                                                                                                                                                                                        30-NOV-2001; 2001WO-US045001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2000; 2000US-0250426P.
Query Match
Best Local Similarity 58.5%
Matches 120; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   07-OCT-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cannule E; CanE partial.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Short J, Mathur EJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DIVE-) DIVERSA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002-557536/59.
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SFYATGTAQAVSEPIDVESHLG-SITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTG 151
                                                                                                                                                                                                                                                                                                                                                                                     09
                                                                                                                                                                                                                                                                                                            SFYATGTAQAVSEPIDVESHLG-SITPAAGAQGSDDIGYAIVWIXDQVNDVKLKVTLRNA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chimeric polypeptide comprising a first domain comprising a cannulae polypeptide and a second domain comprising a heterologous polypeptide or peptide useful for selecting and purifying chiral compositions from
acid sequence represents the Pyrodictium abyssi Cannule E (CanE) partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          second domain having a heterologous polypeptide or peptide. The polypeptides, nanotubule and methods are useful for identifying, separating and synthesizing proceins or ligands, and for selecting and purifying chiral compositions from racemic mixtures. The nanotubule is useful for cells to exchange metabolites, genetic information or signal compounds. The present sequence represents CanE fusion protein.
                                                                                                                                                                                                                                                                                                                                                                             SFYATGTAEATSEPIDVVSNLNTAIAPAAGAQGSVGIGSITIENKTDVNVVKLKITLANA
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    chimeric cannulae polypeptide; metabolite exchange; signal compound;
                                                                                                                                                                                                                                               37;
                                                                                                                                                                                 Length 124;
                                                                                                                                                                          ; Score 305.5; DB 5; Length 1; Pred. No. 3.8e-22; 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 YTNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 85; 89pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADB46052 standard; protein; 124 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18-FEB-2003; 2003WO-US004828.
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                                                                                                                                                                             29.3%;
                                                                                                                                                                                                          48.88;
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                                                                                                                                                                                                       similarity 48.8 78; Conservative
                                    protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DIVE-) DIVERSA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CanE fusion protein.
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                                                                                                     Sequence 124 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003070961-A1.
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                                                                                                                                                                                                                                                                                                                33
                                                                                                                                                                                                                                                                                                                                                                                                                                                      92
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                                                                                                                                                                      Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADB46052;
                                                                                                                                                                                                                                       Matches
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ADB46652
ADB46652
ADB46652
AND ADB4
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The present invention relates to a new method of producing a polypeptide polymer by self-assembly. The method involves providing a number of polypeptides capable of self-assembly in the presence of a divalent cation and polymerising the polypeptides in the presence of a divalent cation and a template molecule. The invention is useful for delivering a drug to a location in the human or animal body. Polypeptides are useful for encapsulating a molecule. The polymeric separation agent is useful for isolating a chiral compound from a mixture. A nucleic acid is useful for comparing a first sequence to a second sequence, where the first sequence is a nucleic acid, and for identifying a feature in a particular sequence. The polypeptide of the invention is useful in fibres, polymeric separation agents, coating compositions, biochips, nanomechanical compositions, biochips, nanomechanical wince it is sequence represents the Pyrodictium abyesi Cannule D (GanD) partial
                                                     EQLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTG 151
                                                                                             ---0G 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing a polypeptide polymer by self-assembly for use in lubricants and coating compositions, comprises polymerizing polypeptides capable of self-assembly in the presence of a divalent cation and template molecule.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid sequence represents the Pyrodictium abyssi Cannule D (CanD) partial protein of the invention. Note: The specification states that this sequence is encoded by the Pyrodictium abyssi Cannule D (CanD) partial gene (ABK8274) but this sequence only encodes part of the protein (residues 1-10)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    animal body, fibre, polymeric separation agent; coating composition, biochip, nanomechanical component, optical switch; optical wave guide; Cannule D; CanD partial.
Polymer; self-assembly; divalent cation; drug delivery; human body;
                                                                          61 EQLKPYFDYLQIVLKS-VDSN-----BIKAVLSLEKPSAVIILDNEDF----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ϋ́
                                                                                                                                    191
                                                                                                                                                                         --COIDATAYYEAKEGML 124
                                                                                                                                                                                                                                                                                                                                                                                        Pyrodictium abyssi Cannule D (CanD) partial protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chow
                                                                                                                              152 YTNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 9; Page 181; 182pp; English.
                                                                                                                                                                                                                                                                    AAU99738 standard; protein; 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-NOV-2001; 2001WO-US045001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-NOV-2000; 2000US-0250426P
                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DIVE-) DIVERSA CORP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-557536/59.
N-PSDB; ABK88274.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 130 AA;
                                                                                                                                                                       105 GDNQ--
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                                                     92
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29.2%; Score 304.5; DB 5; Length 130;

Query Match

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Gaps

37;

Length 124;

29.3%; Score 305.5; DB 7; Length 1 48.8%; Pred. No. 3.8e-22; ive 14; Mismatches 31; Indels

Conservative

Best Local Similarity Matches 78; Conserv

Query Match

78;

Sequence 124 AA;

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61 QLRPYFKYLIIKLVS-LDSN----GNESEEKGMITLWKPYAVIILDHED-
                                                                                                                                                             CAMP factor, SEQ ID 4.
                                             106 NND---IDGD---
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 255 AA;
                                                                                                                                                                                                                                                                                                               WO2003091437-A1.
                                                                                                                                         29-JAN-2004
                                                                                                                                                                                                                                                                                                                                   06-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                     Potter AA,
                                                                                                                     ADE45056;
                                                                                                                                                                                                                                                          Peptide
                                                                                                                                                                                                                                                                                 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                       ADE45056
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               9
                                                                        QLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTGY 152
                                                                                               ----F 105
                               SFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAE 92
                                                    SFYATGTAQAVSEPIDVVSSLGTLNTAAGAQGKQTLGDITIYAHNDVNITKLKVTLANAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New chimeric polypeptide comprising a first domain comprising a cannulae polypeptide and a second domain comprising a heterologous polypeptide or peptide useful for selecting and purifying chiral compositions from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33 SFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAE 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a chimeric cannulae polypeptide and a second domain having a heterologous polypeptide or peptide. The polypeptides, nanotubule and methods are useful for identifying, separating and synthesizing proteins or ligands, and for selecting and purifying chiral compositions from racemic mixtures. The nanotubule is useful for cells to exchange metabolites, genetic information or signal compounds. The present sequence represents Canb fusion protein.
               Gaps
                                                                                                                                                                                                                                                                           chimeric cannulae polypeptide; metabolite exchange; signal compound;
              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 7; Length 130;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                              TNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML 191
Pred. No. 5.1e-22;
2: Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29.2%; Score 304.5; DB 7;
47.2%; Pred. No. 5.1e-22;
live 22; Mismatches 33;
            22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 84; 89pp; English.
                                                                                                                                                                                         ADB46050 standard; protein; 130 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                       Frey
                                                                                                                                                                                                                                                                                                                                                                        18-FEB-2003; 2003WO-US004828.
                                                                                                                                                                                                                                                                                                                                                                                             15-FEB-2002; 2002US-0357406P.
47.2%;
                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                        щ
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     O'donoghue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
75; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                 (DIVE-) DIVERSA CORP
                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-689787/65.
                                                                                                                                                                                                                                                       CanD fusion protein.
Best Local Similarity
                                                                                                                                                                                                                                                                                                          Pyrodictium abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; ADB46049.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        racemic mixtures.
                                                                                                                                                                                                                                                                                                                             WO2003070961-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 130 AA;
                                                                                                                                                                                                                                  04-DEC-2003
            75;
                                                                                                                                                                                                                                                                                                                                                   28-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                    Barton NR,
                                                                                                                                                                                                              ADB46050;
                                                                         93
                                                                                                                   153
            Matches
                                                                                                                                                                    RESULT 10
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QLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTGY 152

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93

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1 SFYATGTAQAVSEPIDVVSSLGTLNTAAGAQGKQTLGDITIYAHNDVNITKLKVTLANAA 60

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The present invention relates to immunogenic proteins comprising one or more cyclic adenosine monophosphate (CAMP) factor epitopes from more than one bacterial species. The proteins and CAMP factors are useful in detecting Streptococcus antibodies in a biological sample, eliciting an immunological response against streptococcal infections, used in vaccine compositions or as diagnostic reagents or in preventing or treating streptococcal infection which causes mastitis. The proteins are also useful in preventing or treating listeriosis. The present sequence is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 GSD---DIGYAIVWIKDQVNDVKLKVTLR-------NAEQLKPYFKYLQIQIT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 GIDYEKPVNEAITSVE-----KLKISLRANPETVYDLNSIGSRVEALIDVIE--AITFS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S TLAIAGIIASAAALALIAGFATTQSPLNSFYATGTAQAVSEPIDVES-HLGSITPAAGAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New cyclic adenosine monophosphate(CAMP)-3 polypeptide comprising
streptococcal CAMP factor epitopes, useful in treating or preventing
bacterial infection or as vaccine or diagnostic reagent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic; cyclic adenosine monophosphate factor; CAMP factor; mastitis; listeriosis; antibacterial; antiinflammatory; vaccine; immunostimulant; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7; Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84; Indels
                                     ---NQCQ----IDATAYYEAKEGML 130
153 TNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Song X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.2%; Score 96; DB '25.0%; Pred. No. 0.59 tive 31; Mismatches

    .29
    /note= "Signal peptide"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                        ADE45056 standard; protein; 255 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 7; Fig 3; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-APR-2003; 2003WO-CA000587.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-APR-2002; 2002US-00134021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perez-Casal J,
                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYSA-) UNIV SASKATCHEWAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
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New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
   ---VLDKEDIAVLYPDKTGYT 153
                  TOHLTNKVSOANIDMGFGITKLVIRILDPFASVDSIKAQVNDVKALEQKVLTYPDIKPTD 181
                                                                                                                                                                                 Antisense; prokaryotic essential gene; cell proliferation; drug design.
                                                                                                                                                                                                                                                                                                                                                             Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                             ŖŖ
                                                                                                                                                                                                                                                                                                                                                             Ohlsen Forsyth
                                                                                                                                                              Protein encoded by Prokaryotic essential gene #18831,
  SGYETNSTALGN ----FSETKAVISLDNPSAVI----
                                                                                                                                                                                                                                                                                                                                                            Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 61228; 1766pp; English.
                                                  :|: :|| | :|
182 RATIYTKSKLDKEI-WNTRFTRDKKVLNVKEF
                                     154 NTSIWVPGEPDKIIVYNE--TKPVAILNFKAF
                                                                                                     ABU33304 standard; protein; 322 AA
                                                                                                                                                                                                                                                                                                                                                            Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                        06-SEP-2001) 2001US-00948993.
25-OCT-2001) 2001US-0342923P.
                                                                                                                                                                                                                                                            21-MAR-2002) 2002WO-US009107.
                                                                                                                                                                                                                                                                                                           08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                              21-MAR-2001/ 2001US-00815242
                                                                                                                                                                                                                                                                                                                                                            Malone
                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                    Legionella pneumophila.
                                                                                                                                                                                                                                                                                                                                                          Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                       2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ACA37174
                                                                                                                                                                                                                       WO200277183 - A2
                                                                                                                                                                                                                                                                                                          08-FEB-2002;
                                                                                                                                            19-JUN-2003
                                                                                                                                                                                                                                         03-OCT-2002
                                                                                                                          ABU33304;
 107
                                                                                                                                                                                                                                                                                                                                                          Wang L,
Wall D,
                                                                                   RESULT 12
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the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid nucleic acid antisense expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the gene product or that has an activity against a biological pathway trequired for proliferation, or that inhibits cellular proliferation (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or the gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense mucleic acids are useful for identifying proteins or screening for homologous nucleic acids required
invention relates to an isolated nucleic acid comprising any one of
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                 drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is encoded by one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                      67 NDNYSTDTSQSYDEPALVKEDRSTISDNAK------LIDKIQQLQKEIQELKG 113
                                                                                                                                                                                                                                                                                                                                              91 AEQLKPY-FKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVL---DKEDIAVLY 146
                                                                                                                                                                                                                                                                                                                                                                                114 OLEVOAHDLKILQQQQVAFYKDLDSRLSNSSTSAKIVQNDKPATDISLGSNSPETLKVAS 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae; group A streptococcus; Streptococcus pyogenes; antibacterial; antiinflammatory; infection; vaccine; meningitis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a protein (ABP25413-ABP30895) from group B streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in the specification. The proteins have antibacterial and antiinflammatory
                                                                                                                                                                                                                                                                        32 NSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKV-TLRN 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Streptococcus protein for the treatment or prevention of infection or
cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease caused by Streptococcus bacteria, such as meningitis, and for detecting a compound that binds to the protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fraser C;
                                                                                                                                                                                                                                                                                                                                                                                                                    147 PD-KTGYTNTSIWVPGEPDKIIVYNETKPV-AILNFKAFYEAKEGMLFD 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                      174 POIKAGSSN-----GKPQPVVAVSRANPADEQISYLAAYELVKNKRYD 216
                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Margarit Y RosI, Grandi G,
                                                                                                                                                                                                                                        71;
                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                      34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptococcus polypeptide SEQ ID NO 10746.
                                                                                                                                                                                                  8.8%; Score 92; 22.5%; Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 4181; 4525pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ABP30785 standard; protein; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-OCT-2000; 2000GB-00026333.
24-NOV-2000; 2000GB-00028727.
07-MAR-2001; 2001GB-00005640.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001WO-GB004789.
                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus agalactiae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Masignani V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2002-352536/38.
                                                                                                                                                                                                                 Local Similarity
les 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHIR-) CHIRON SPA
                                                                                                                                                                Sequence 322 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ABN71416.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200234771-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-JUL-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAY-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Telford J,
Tettelin H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABP30785;
                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GENO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disease
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Matches
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activity. (I), nucleic acids encoding (I), ABN66044-ABN71526 and antibodies that bind (I) are used in the manufacture of medicaments for the treatment or prevention of infection or disease caused by Streptococcus bacteria, particularly S. agalactiae and S. pyrogenes. Nucleic acids encoding (I) are used to detect Streptococcus in a biological sample. (I) is used to detectine whether a compound binds to (I). A composition comprising (I) or a nucleic acid encoding (I), may be used as a vaccine or diagnostic composition. The disease caused by Streptococcus that is prevented or treated may be meningitis. Nucleic acid encoding (I) may be used to recombinantly produce (I) and may be used in gene therapy. Antibodies to (I) are used for affinity chromatography, immunoassays, and distinguishing/identifying
                                                                                                                                                                                                                                                                                                                                                                     Streptococcus proteins
         $55555555555555X8
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Sequence 255 AA;

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-NAEQLKPYFKYLQIQIT 106
                                                                                                                                                                                                                     GTDYEKTVNEALTSVE-----KLKTSLRANPETVYDLNSIGSRVEALTDVIE--ALTFS 121
                                                                                                                                                                                                                                                              107 SGYETNSTALGN----FSETKAVISLDNPSAVI-----VLDKEDIAVLYPDKTGYT 153
                                                                                                                                                                                                                                                                                                       TQHLANKVSQANIDMGFGITKLVIRILDPFASVDSIKAQVNDVKALEQKVLTYPDLKPTD 181
                                                                                    5 TIAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVES-HLGSITPAAGAQ 63
                                                                                                                               12 TLVAGALLFSPAVLEVHADOVTTPQVVNHVNSNNQAQQMAQKLDQDSIQLRNIKD--NVQ
                                                           Gaps
                                                        44;
Query Match

8.7%; Score 91; DB 5; Length 255;
Best Local Similarity 24.5%; Pred. No. 1.8;
Matches 52; Conservative 31; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                182 RATIYTKSKLDKEI-WNTRFTRDKKVLNVKEF 212
                                                                                                                                                                                                                                                                                                                                                     154 NTSIWVPGEPDKIIVYNE--TKPVAILNFKAF 183
                                                                                                                                                                          64 GSD---DIGYAIVWIKDQVNDVKLKVTLR----
                                                                                                                                                                                                                                                                                                         122
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ADC51492 standard; protein; 978 AA 18-DEC-2003 ADC51492; RESULT 14 ADC51492 

(first entry)

Bacterial beta-hexosaminidase gene SEQ ID NO:8.

beta-hexosaminidase; beta-glucosidase; sphingo-glycolipid.

Paenibacillus sp.

JP2003061663-A.

04-MAR-2003.

21-AUG-2001; 2001JP-00249782.

21-AUG-2001; 2001JP-00249782.

(SANG-) SANGAKU RENKEI KIKO KYUSHU KK.

WPI; 2003-691955/66. N-PSDB; ADC51491 Novel exo-type ganglioside degradation enzymes e.g. beta- glucosidase and beta-hexosaminidase, useful for producing sphingoglycolipids, are derived from Paenibacillus species of strain TS12 FERM P-18416.

Claim 4; SEQ ID NO 8; 23pp; Japanese.

The invention relates to a novel recombinant polypeptide, encoded by beta - hexosaminidase gene derived from Paenibacillus sp. or encoded by beta-glucosidase gene derived from Escherichia coli. A gene of the invention

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                                                                                                                                                                               107
                                                                                                                                                                                                                   528
                                                                                                                                                                                                                                                         163
                                                                                                                                                                                                                                                                                     529 GY-LNGTLVGGAKWTAGKQGNGVSFDGSSGYİNLGGQDİ-----TGNWTAAVWVYGQP 580
                                                                                                                                                                     48 DVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITS
                                                                                                                                                                                                           477 DFKERLIEHTPRLONKGIKFFADPIVW-----ELPIVQINSEWKMDEGTGTVVKDTS
is useful for producing sphingo- glycolipids. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                   108 GYETNSTALGNFSETKAV----ISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEP
                                                                                                                                           Gaps
                                                                                                                                           39;
                                                                                                                                                                                                                                                                                                                               ----KIIVYNETKPVAILNFKAFYEAKEGMLFDSLP 196
                                                                                                                                                                                                                                                                                                                                                                 581 NTINNETLLSGTTSAIKINQYNKTGKVGI----TIYGTKDYTYNYSIP 624
                                                                                                 DB 7; Length 978;
                                                                                                                                       69; Indels
                                                                                                                                     17; Mismatches
                                                                                               8.4%; Score 87.5; I
25.6%; Pred. No. 28;
                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                             164 D-----
                                                                                                             Local Similarity
les 43; Conserv
                                                         Sequence 978 AA;
                                                                                         Query Match
Best Local 9
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ABB57211 standard; protein; 284

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ABB57211;

(first entry) 07-MAR-2002

Mouse ischaemic condition related protein sequence SEQ ID NO:514.

Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.

Mus musculus.

WO200188188-A2

22-NOV-2001.

18-MAY-2001; 2001WO-JP004192.

18-MAY-2000; 2000JP-00145977.

(UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.

Ishii Y; Takahashi Y, Nagata T, Asai S, Ishikawa K,

WPI; 2002-034733/04. N-PSDB; ABI99523.

measuring Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or determining the expression profile of a gene group comprising these genes. 

Claim 2; Page 1418-1419; 2690pp; English.

The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (1) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compressive expression levels of particular genes (AB199202 to AB199912, encoding the expression levels of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The expression complete of a gene group comprising these genes. The expression indicator when screening for ischaemic condition-improving drugs or the captures for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention

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Sequence 284 AA;
XX
So
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1 VKYTILAIAGIIASAAALALIAGFATTQSPLNSFYATGT---AQAVSEPIDVESHLGSIT 57 Query Match 8.3%; Score 86.5; DB 5; Length 284; Best Local Similarity 26.2%; Pred. No. 6; Matches 45; Conservative 28; Mismatches 68; Indels 31; Gaps

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qq

Search completed: April 6, 2004, 12:38:53 Job time : 62 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 6, 2004, 11:43:46 ; Search time 22 Seconds

(without alignments) 485.753 Million cell updates/sec

US-09-997-807-2 score:

1042 1 VKYTTLAIAGIIASAAALAL.......EGMLFDSLPVIFNFQVLQVG 207 Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 seqs, 51625971 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

/cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
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/cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pep:\* Issued\_Patents AA:\* 

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### CITIMMADITE

Description	SUMMARIES SUMMARIES SUMMARIES  US-09-543-681A-8284 Sequence 32. US-09-145-32467 Sequence 32. US-09-107-532A-4072 Sequence 32. US-09-107-532A-4072 Sequence 12. US-09-107-537-4 US-09-657-440-12 US-09-657-440-12 Sequence 12. US-09-657-440-12 Sequence 12. US-09-657-440-12 Sequence 12. US-09-657-440-12 Sequence 23. US-09-105-537-4 Sequence 24. US-09-105-537-4 Sequence 12. US-09-489-039A-12174 Sequence 13. US-09-489-039A-13379 Sequence 13. US-09-481-786-1 Sequence 13. US-09-481-786-1 Sequence 12. US-09-441-786-1 Sequence 12. US-09-441-786-1 Sequence 12. US-09-543-681-786-1 Sequence 12. US-09-841-786-1 Sequence 12. US-09-841-786-1 Sequence 12. US-09-841-786-1 Sequence 27. US-09-489-039A-131-786-1 Sequence 12. US-09-841-786-1 Sequence 27. US-09-841-786-1 Sequence 27. US-09-484-340-23 Sequence 27. US-09-384-361-34 Sequence 34.	Length DB ID Description 100				, r	, ' n' n'	455030	4	٨	Appl	Appl	Appl	Ann	1,100	Appl	Appl	4 4		١.	2. A	(2	ppli	Ap	Appl	poli	ppli	Appl	Appl	Appl	4
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GENERAL INFORMATION:
APPLICANT: MARC J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

; Sequence 32467, Application US/09252991A ; Patent No. 6551795

US-09-252-991A-32467

Sequence 264, App	Sequence 7, Appli	Sequence 7, Appli	7	258	Sequence 262, App	Sequence 266, App	Sequence 5999, Ap		30,	616	30, 7	m	32.		2061		
US-09-071-035-264	US-08-194-290-7	US-08-614-377A-7	US-09-142-648B-7	US-09-071-035-258	US-09-071-035-262		US-09-134-000C-5999	US-09-813-659-30	US-09-549-067A-30	US-09-543-681A-6165	US-08-121-054C-30	US-08-539-436-30	US-09-813-659-32	US-09-549-067A-32	US-09-252-991A-20610	US-09-252-991A-28459	US-09-252-991A-17263
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699	1026	1026	1026	1638	1638	1638	1747	274	274	291	302	302	302	302	399	728	1251
7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2	7.2
26	92	16	9/	97	92	97	26	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5	75.5
<b>c</b> co	6	30	11	22	33	34	35	36	3.7	38	39	0	Į	12	13	14	12

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APPLICANT: GARY BRETON

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABI

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

CURRENT APPLICATION NUMBER: US/09/543,681A

CURRENT APPLICATION NUMBER: US 60/128,706

PRIOR FILING DATE: 1999-04-09

NUMBER OF SEQ ID NOS: 8344

SEQ ID NO 9284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       130 SRHVLILIDGVRTNQAGISGSYDMSQL-----PLSLVQRIEYIRGPRSAVYGSDAIGGVI 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73 VWIKDQVNDVKLKVTLRNAEQLKPYFKYL-QIQITSGYETNSTALGNFSETKAVISLDNP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 SAVIVLDKEDIAVLYPDKTGYTNTSIW-----VPGE 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14 SAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSIT-PAAGAQGSDDIGYAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.1%; Score 105; DB 4; Length 651; 22.0%; Pred. No. 0.013; Live 27; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             163 PDKIIVYNETKPVAILNFKAFYEAKEGMLFDSLPVIFN 200
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ALIGNMENTS
                                                                                                            Sequence 8284, Application US/09543681A Patent No. 6605709 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Proteus mirabilis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Conservative
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Matches 48; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                   37 ARIAALGILIPLAAGSAVAAEEGSSVKDAAKA-AVSSAÌETGKNLIGGVSEGITSGRQSA 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      --OSPLNSFYATGTAQAVSEPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 ---LGNFSETKAVISLDNP----SAVIVLDKEDIAVLYPDKTGYTNTSIWVPG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 TVRLINLIQIGALLVIDNDGYSNALVALANPDDVTV--PAKAGIRQIFVFEGG 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74;
                                                                                                                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                          9 AGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDV-ESHLGSIT---
                                                                                                                                                                                                                                                                                     9.0%; Score 94; DB 4; Length 208; 26.6%; Pred. No. 0.035; cive 27; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 83; DB 4; Length 626; [9.5%; Pred. No. 3.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 KEDI---AVLYPOKTGYTNTSIWVPG---EPDKIIVYNETK 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Kaufmann, Stefan
APPLICANT: Kaufmann, Stefan
APPLICANT: Hess, Jrgen
TITLE OF INVENTION: Tuberculosis Vaccine
FILE REFERENCE: 16862PUS
CURRENT APPLICATION NUMBER: US/09/485,717
CURRENT APPLICATION NUMBER: EP 97114614.7
PRIOR APPLICATION NUMBER: EP 97114614.7
PRIOR APPLICATION NUMBER: PS 97114614.7
PRIOR APPLICATION NUMBER: PCT/EP98-05109
PRIOR FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
CURRENT APPLICATION NUMBER: US/09/252,991A CURRENT FILING DATE: 1999-02-18 PRIOR APPLICATION NUMBER: US 60/074,788 PRIOR FILING DATE: 1998-02-18 PRIOR APPLICATION NUMBER: US 60/094,190 PRIOR FILING DATE: 1998-07-27 NUMBER OF SEQ ID NOS: 33142
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Patent No. 6673353
GENERAL INFORMATION:
                                                                                                                                                                                                                  ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                              46; Conservative
                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                  SEQ ID NO 32467
LENGTH: 208
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LENGTH: 626
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                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 46
                                                                                                                                                                                                  TYPE: PRT
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Sequence 4072, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 VKLK--VTLRNAEQLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLD- 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85 KRLEWVATISSGS-----TYTYYPDSVK-GRFT----ISRDNAKDTLYLOM 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22 AGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 ASSSVSSSYLHWFQQKSIAKAFKNGGDLVKPGGSLKCSCAASGFTFISYGMSWVR-QTPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35; Gaps
                                                                                                                     Patent No. 5455030

Patent No. 5455030

Patent No. 100 No. 5455030

Patent No. 100 No. 5455030

Patent No. 5455030

Patent No. 5455030

Patent No. 5455030

Polypeptide Binding Molecules

NUMBER OF SEQUENCES: 24

CURRENT APPLICATION DATE: 14

PATENT APPLICATION NUMBER: 105 (8/40,440)

PATENT APPLICATION NUMBER: 512,910

PATENT APPLICATION NUMBER: 512,910

PATENT NUMBER: 52-AR-1990

PAPLICATION NUMBER: 52,409,617

PATENT NUMBER: 92,110

PATENT NUMBER: 92,10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 SGLKSEDTAMYYCARRITTVVLTDYYAMDYWGPGSP-KLWIYS 167
180 SELVENQPDVLPVKRDSLTLSIDLPGMTNQDNKIVVKNATK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
7.7%; Score 80.5; DE
Best Local Similarity 24.5%; Pred. No. 1.2;
Matches 40; Conservative 22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: CD/ROM ISO9660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: Massachusetts
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 225
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                                                                           RESULT 4
5455030-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 SEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKD--QVNDVKLKVTLRNAEQLKPYFKYL 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 SEQLDNQGH-----EKQEGVNGAKFSVYDVSDILQKMDVKDLTTDQIESQLKDRVKKL 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 ---QIQITSGYETNS----TALGNFS-----ETKAVISLDNPSAVIVLDKEDIAVLYP- 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148 -DKTGYTNTSIWV-----PGEPDKIIVYNETKPVAILNFKAFYE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         204 SDKNGEFLKDVWIYPKSEASQPKEEVKKIVSTGVK-----KNFFE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.7%; Score 80.5; DB 4; Length 256; 25.7%; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 300622002120
CURRENT APPLICATION NUMBER: US/09/320,878A
CURRENT FILING DATE: 1999-05-27
EARLIER APPLICATION NUMBER: CIP OF 09/141,908
EARLIER FILING DATE: 1998-06-28
EARLIER FILING DATE: 1998-06-28
EARLIER FILING DATE: 1998-06-28
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1998-06-06
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: CIP OF 08/846,247
EARLIER FILING DATE: 1999-02-08
EARLIER APPLICATION NUMBER: 60/119,139
EARLIER APPLICATION NUMBER: 60/110,880
EARLIER FILING DATE: 1999-02-08
EARLIER FILING DATE: 1999-02-28
EARLIER FILING DATE: 1998-03-22
EARLIER FILING DATE: 1998-05-28
NUMBER OF SEQ ID NOST: 34
SOFTWARE: PATCHILL Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...256
SEQUENCE DESCRIPTION: SEQ ID NO: 4072;
                                              GTC-012
Pamela Deneke
                                                                                                                                                                                                                                                                                                                           ORGANISM: Enterococcus faecium
                 REGISTRATION NUMBER: 40,489
REPERENCE DOCKET WUMBER: GT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-8077
INFORMATION FOR SEQ ID NO: 4072:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                LENGTH: 256 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 12, Application US/09320878A Patent No. 6117659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary C.
APPLICANT: MCDANIEL, RObert
APPLICANT: TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 25.79
Matches 43; Conservative
NAME: Ariniello,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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US-09-320-878-12
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TITLE OF INVENTION: Combinatorial Polyketide Libraries Produced Using a TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
TITLE OF INVENTION: Modular PKS Gene Cluster as Scaffold
CURRENT APPLICATION NUMBER: US/09/141,908
EARLIER APLICATION NUMBER: CIP OF 09/073,538
EARLIER PILING DATE: 1998-05-06
EARLIER PILING DATE: 1998-05-06
EARLIER PILING DATE: 1998-01-05
EARLIER PILING DATE: 1998-01-05
EARLIER PILING DATE: 1998-01-05
EARLIER PILING DATE: 1998-01-05
EARLIER PILING DATE: 1998-05-28
NUMBER: OF SEQ ID NOS: 31
                                                                                                                                                                                                                                                                               428 AVRATGGYÄTVÖLGSHTIEAGQVYGKVSSPLLKLTKGTHKLTISGFAMSATPLSLELGWV 487
                                                                                                                                                                                                                                 76 KDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTAL-GNFSETKAVISLDNPSAV 134
                                                                                                                                                                                                                                                                                                                                                                       135 IVLDKEDIAVLYP--DKTGYTNTSIWVPG----EPDKIIVYNETKPVAILNFKAFYEAKE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           135 IVLDKEDIAVLYP--DKTGYTNTSIWVPG----EPDKIIVYNETKPVAILNFKAFYEAKE 188
                                                                                               17 ALALLAGFATTQSPLNSFYATGTAQAVSEP-IDVESHLGSITPAAGAQGSDDIGYAIVWI 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17 ALALLAGFATTQSPLNSFYATGTAQAVSEP-IDVESHLGSITPAAGAQGSDDIGYAIVWI
                                   23; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   548 VVLNTGS-SVLMPWLSKTRAV-LDMWYPGQAGABATAALLYGDVNP-----
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                               Indels
                               97;
Best Local Similarity 19.8%; Pred. No. 11; Matches 38; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 10, Application US/09141908; Patent No. 6503741; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Streptomyces venezuelae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C.
APPLICANT: BETLACH, Mary
APPLICANT: MCDANIEL, Robert
APPLICANT: TANG, LEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 769
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US-09-141-908-10
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RESULT

7.6%; Score 79.5; DB 3; Length 769;

Query Match

547 TPAAADATIAKAVESARKARTAVVFAYDDGTEGVDRPNLSLPGTQDKLISAVADANPNTI

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 ALALLAGFATTQSPLNSFYATGTAQAVSEP-IDVESHLGSITPAAGAQGSDDIGYAIVWI 75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23;
                                                                                                                                                                                                   TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE FILE REPERENCE: 30062203120
CURRENY APPLICATION NUMBER: US/09/657,440
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR APPLICATION NUMBER: 09/320,878
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR APPLICATION NUMBER: CIP OF 09/141,908
PRIOR PILING DATE: 1999-08-28
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 7.6%; Score 79.5; DB 3; Length 809; Best Local Similarity 19.8%; Pred. No. 11; Matches 38; Conservative 34; Mismatches 97; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Sherman, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin
FILE REPERENCE: 600.4380S1
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT APPLICATION NUMBER: US/09/105,537A
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         548 VVLNTGS-SVLMPWLSKTRAV-LDMWYPGQAGAEATAALLYGDVNP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34; Mismatches 97; Indels
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7.6%; Score 79.5; DB 4;
Best Local Similarity 19.8%; Pred. No. 11;
Matches 38; Conservative 34; Mismatches 97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-105-537-24
; Sequence 24, Application US/09105537A
; Patent No. 6265202
                     Seguence 12, Application US/09657440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Streptomyces venezuelae
US-09-105-537-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Streptomyces venezuelae
                            Sequence 1. Organization Sequence Applicant: APPLICANT: ASHLEY, Gary
APPLICANT: BETLACH, Melanie C. APPLICANT: BETLACH, Mary C. APPLICANT: TANG, Li APPLICANT: TANG, Li
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GMLFDSLPVIFN 200
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US-09-657-440-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 12
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APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
APPLICANT: Buchbinder, Jenny
TILE RUNDENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REPERRICE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT APPLICATION NUMBER: 100/10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
SUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10;
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135 IVLDKEDIAVLYP--DKTGYTNTSIWVPG----EPDKIIVYNETKPVAILNFKAFYEAKE 188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           498 VIIQNLMPATVIFRVMAQNKHGSGESSAPLR--VETQPEVQLPGPA----
                                    543 -PNLRAYA-----ASPTSITVTWET-PVSGNGEIONYKLYYMEK 579
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shearan, D.H.
APPLICANT: Liu, H.
APPLICANT: Liu, H.
APPLICANT: Xue, Y.
APPLICANT: Zhao, L.
TITLE OF INVENTION: DNA encoding methymycin and pikromycin CURRENE 600, 438021.
CURRENT APPLICATION NUMBER: US/09/105,537A
CURRENT FILING DATE: 1998-06-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1730175CD1
US-09-976-594-531
                                                                                                                                                                                                                                                                                      ; Sequence 531, Application US/09976594; Patent No. 6673549; GENERAL INFORMATION:
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Best Local Similarity 22.1%;
                                                                                                         189 GMLFDSLPVIFN 200
                                                                                                                                                              652 GKLTQSFPAAEN 663
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
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1552 AVRATGGYATVQLGSHTIEAGQVYGKVSSPLLKLTKGTHKLTISGFAMSATFLSLEIGWV 1611
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                                                                                                                                                                                                                                                      17 ALALLAGFATTQSPLNSFYATGTAQAVSEP-IDVESHLGSITPAAGAQGSDDIGYAIVWI 75
                                                                                                                                                                                                              23;
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Patent No. 6056953
GENERAL INFORMATION:
APPLICANT: Lesile Hickle
APPLICANT: Jewel Payne
TITLE OF INVENTION: Materials and Methods for the Control of
TITLE OF INVENTION: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                       Length 3782;
                                                                                                                                                                                                            97; Indels
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,024
                                                                                                                                                                  7.6%; Score 79.5; DB 3;
19.8%; Pred. No. 1.3e+02;
tive 34; Mismatches 97;
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2421 N.W. 41st Street, Suite A-1
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FastSEQ for Windows Version 3.0
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FILLING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: SALIWANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA79
TELECOMMUNICATION INFORMATION:
THE REPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,226
                                                                                                       ORGANISM: Streptomyces venezuelae
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INFORMATION FOR SEQ ID NO: 28;
SEQUENCE CHARACTERISTICS;
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                                                                                                                                                                                                              38; Conservative
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STRANDEDNESS: single
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FL
                                                                                                                                                                                        Best Local Similarity
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US-09-224-024-28
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                                                           LENGTH: 3782
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                                           SEQ ID NO 4
                                                                                                                                                                       Query Match
                                                                                   TYPE: PRT
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Fax number: . (619)453-6991
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                                                                                                                                        520 FAWTHSSVDPKNTIYTHLTTQ1---PAVKANSLG--TASKVVQGPGHTGGDLIDFKDH-- 572
                                                                                                                                                                                                                                                                  -----SAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIV 168
                                                                                                                                                                                                                                                                                             619 NPTFSGTDYTNLKYXDFQYLEFSNEVKFAPNQNISLVFNRSDVYTNTTVLI----DKI--- 672
                                                                                             24 FATTQS---PLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVN. 80
                                                     68; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Materials and Methods for the Control of TITLE OF INVENTION: Calliphoridae Pests
DB 3; Length 1180;
23;
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                                                     66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4980 Carroll Canyon Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
                                                                                                                                                                                                                                                                                                                                                       169 YNETKPVAILNFKAFYEAKEGMLFDSLPVIFN 200
                                                                                                                                                                                                                                                                                                                                                                                               673 --EFLPIT----RSIREDREKOKLETVOQIIN 698
        Query Match (7.6%; Score 79; DB 3; Best Local Similarity 22.2%; Pred. No. 23; Matches 47; Conservative 31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S: David R. Saliwanchik
2421 N.W. 41st Street, Suite A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (619) 453-8030
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GENERAL INFORMATION:
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State/Province:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Street address:
City: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Saliwanchik, David R. REGISTRATION NUMBER: 31,794
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Postal code/Zip:
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Telex number:
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
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APPLICANT:
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APPLICANT:
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LENGTH: 408
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APPLICANT: Gary Breton et. al
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
TITLE OF INVENTION: PREUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US,09/489,039A
CURRENT FILING DATE: 1099-01-27
PRIOR APPLICATION NUMBER: US,60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 13379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 12174, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : : : : : : | | : : | | : : | 1. | : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | :
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                                                                           520 FAWTHSSVDPKNTIYTHLTTQI---PAVKANSLG--TASKVVQGPGHTGGDLIDFKDH-- 572
                                                                                                                                                                                                                                                                                                                                   --SAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIV 168
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FATTQS---PLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVN 80
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CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12174
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57; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 FALOLSAEGKTLYVSNSIDGGISAIDTATGKVKNRLLFSERNEKGRPYGARQILLIANNTL 207
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                                                                                                                                                                                                                                                   ----SAVSQPV-VDSPVPNV
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                                                                                                                                                    73; Indels 138; Gaps
                                                                                                 7.5%; Score 78; DB 4; Length 408; 22.2%; Pred. No. 5.7;
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                                                                                                                                                    69; Conservative 31; Mismatches
                                                                                                                                                                                                                                                        49 MKYTLPALTLAIS-----AALSGCATPHS
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TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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                                                                                                                            Best Local Similarity
                                                US-09-489-039A-13379
                                                                                                                                                                                                                                                                                                            54
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                                                                                                    Query Match
                                                                                                                                                       Matches
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein April 6, 2004, 12:33:31; Search time 42 Seconds (without alignments) 1294.407 Million cell updates/sec Run on:

US-09-997-807-2 1042 1 VKYTTLAIAGIIASAAALAL.......EGMLFDSLPVIFNFQVLQVG 207 Title: Perfect score:

**BLOSUM62** Scoring table: Sequence:

1071772 seqs, 262633353 residues Gapop 10.0 , Gapext 0.5 Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

Published Applications AA:\*

| Cgn2\_6/ptodata1/pubpaa/US07\_PUBCOMB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US07\_PUBCOMB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US06\_PUBF\_PUB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US06\_PUBF\_PUB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US07\_NEW\_PUB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US08\_PUBCOMB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US08\_PUBCOMB.ppp:\*
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| Cgn2\_6/ptodata1/pubpaa/US10A\_PUBCOMB.ppp:\*
| Cgn2\_6/ptodata1/pubpaa/US10B\_PUBCOMB.ppp:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 4, Appli Sequence 61228, A Sequence 34, Appl Sequence 1972, Ap Appli Appli Appli Sequence 2, Appli Sequence 10, Appl Sequence 10, Appl Sequence 8, Appli Sequence 4, At Sequence 6, At Sequence 6, At Sequence 12, A Sequence 12, A Sequence 8, At At Sequence 8, At At At Sequence 8, At At Sequence 8, At At Sequence 8, At At Sequence 8, At Seq Description Sequence Sequence US-10-282-122A-61228 US-09-893-519A-34 US-10-369-493-1972 US-09-997-807-2 US-10-370-370-4 US-09-997-807-4 US-09-997-807-4 US-09-997-807-6 US-10-370-370-4 US-10-370-370-12 US-10-370-370-12 US-09-997-807-10 US-09-997-807-10 US-09-997-807-10 Query Match Length DB  $\begin{array}{c} 0.000\\ 0.$ 473 307.5 305.5 305.5 304.5 96.5 86.5 1042 1042 553.5 553.5 540 Result

Appl

	Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl Sequence 24, Appl
US-10-412-699B US-10-374-780A US-10-108-260A US-10-108-260A US-09-919-48-722-2 US-09-919-4780A US-10-171-404A US-10-374-780A US-10-382-122A US-10-38-122A US-10-38-599- US-10-335-977- US-10-335-977- US-10-335-977- US-10-335-977- US-10-335-977- US-10-335-977- US-10-335-977- US-10-335-977- US-10-335-977- US-10-38-626-6 US-10-282-122A US-10-282-122A US-10-282-122A US-10-38-493- US-10-38-493- US-10-38-493- US-10-38-493- US-10-38-122A US-10-38-122A US-10-38-122A	US-09-861-289-24 US-09-860-846-24 0 US-09-888-384B-24 0 US-09-836-821-24
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#### ALIGNMENTS

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61 GAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKFYFKYLQIQITSGYETNSTALGNFS 120
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                                        Sequence 2, Application US/09997807

Sequence 2, Application US/09997807

Publication No-052003019869431

Seberal Information:
APPLICANT: UN Action Laffgrey
APPLICANT: We michael Laffgrey
APPLICANT: We michael Laffgrey
APPLICANT: Kevin Chew
TITLE OF INVENTION: Method of Making A Protein Polymer
TITLE OF INVENTION: Uses of the Polymer
FILE REFERENCE: DVSA-1005US
CURRENT APPLICATION NUMBER: US/09/997,807

CURRENT FILING DATE: 2001-11-30

PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 207
TYPE: PRT
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Best Local Similarity 100.0
Matches 207; Conservative
RESULT 1
US-09-997-807-2
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ETKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIMVPGEPDKIIVYNETKPVALLNF 180
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                                                                                                                                                                                                                                                                             APPLICANT: Barton, Nelson R.
APPLICANT: Barton, Nelson R.
APPLICANT: O'Donoghue, Eileen
APPLICANT: O'Donoghue, Eileen
TITLE OF INVENTION: THEM AND WETHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 0.9010-11501
CURRENT APPLICATION NUMBER: US/10/370,370
CURRENT FILING DATE: 2003-02-18
PRIOR APPLICATION NUMBER: 6/357,406
PRIOR PILING DATE: 2002-02-15
SOFTWARE: FREESE OF TWINGOWS Version 4.0
SEQ ID NO 2
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APPLICANT: Eric J. Mathur
APPLICANT: Eric J. Mathur
APPLICANT: W. Michael Lafferty
APPLICANT: W. Michael Lafferty
APPLICANT: Welson Barton
TITLE OF INVENTION: Method of Making A Protein Polymer
TITLE OF INVENTION: Wese of the Polymer
FILE REFERENCE: DVSA-1005US
CURRENT APPLICATION NUMBER: US/09/997,807
CURRENT APPLICATION NUMBER: US/09/997,807
CURRENT APPLICATION NUMBER: 60/250,426
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 1042; DB 15;
100.0%; Pred. No. 1.8e-101;
live 0; Mismatches 0;
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                                                                                           181 KAFYEAKEGMLFDSLPVIFNFQVLQVG 207
                                                                  181 KAFYEAKEGMLFDSLPVIFNFQVLQVG 207
                                                                                                                                                                                                             ; Sequence 2, Application US/10370370; Publication No. US20040006778A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/09997807; Publication No. US20030198681A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Pyrodictium abyssi
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Best Local Similarity 100.
Matches 207; Conservative
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US-10-370-370-2
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Sequence 4, Application US/10370370

Sequence 4, Application US/10370370

Sequence 4, Application US/10370370

Publication No. US20040006778A1

APPLICANT: Barton, Nelson R.

APPLICANT: Barton, Nelson R.

APPLICANT: Prey, Gerhard

TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM

FILE REFERENCE: 09010-115001

CURRENT APPLICATION NUMBER: US/10/370,370

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION UMBER: 60/357,406

FRIOR APPLICATION UMBER: 60/357,406

FRIOR FILING DATE: 2002-02-15
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                                                                                                                                                                                                                                                                                                               61 GAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNFS 120
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                                                                                                                                             Gaps
                                                                                                                                          37;
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                                                                                    DB 10; Length 170;
                                                                                 53.1%; Score 553.5; DB 10; Length 60.2%; Pred. No. 4.4e-50; tive 12; Mismatches 33; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
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ORGANISM: Pyrodictium abyssi
ORGANISM: Pyrodictium abyssi
US-09-997-807-4
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                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       27; Indels 36; Gaps
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Publication No. US2004006778A1

Publication No. US2004006778A1

APPLICANT: Barton, Nelson R.

APPLICANT: O'Donoghue, Eileen

APPLICANT: C'DONOGhue, Eileen

TITLE OF INVENTION: CHIMERIC CANNULAE PROTEINS, NUCLEIC ACIDS ENCODING

TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM

CURRENT APPLICATION UNBER: US/10/370,370

CURRENT FILING DATE: 2003-02-18

PRIOR APPLICATION NUMBER: 60/357,406

WINNERD OF COL TAXED OF COL 202-02-15
                                                                                                                                                                                                                                                                                                                                                                                                51.8%; Score 540; DB 10; Length 178; 58.5%; Pred. No. 1.3e-48; ive 22; Mismatches 27; Indels 3
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                                                                             APPLICANT: Kevin Chow
TITLE OF INVENTION: Method of Making A Protein Polymer and
TITLE OF INVENTION: Uses of the Polymer
FILE REFERENCE: DVSA-1055US
CURRENT APPLICATION NUMBER: US/09/997,807
CURRENT FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 6/250,426
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 10
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SOFWARR: FastSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 178
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                          Eric J. Mathur
W. Michael Lafferty
Nelson Barton
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Best Local Similarity
Matches 120; Conserv
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APPLICANT: Jay Short
                                                                                                                                                                                                                                                                                               TYPE: PRT
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                                          APPLICANT:
APPLICANT:
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                                                                                                             120 SETKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGGEPDKIIVYNETKPVAILN 179
                                                                                                                                                                         ---YDSTNKIQ-LK 145
60 AGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNF 119
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Sequence 8, Application US/10370370
Publication No. US20040006778A1
GENERAL INFORMATION:
APPLICANT: Barton, Nelson R.
APPLICANT: O'Donoghue, Eileen
APPLICANT: FLEV, Gerhard
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
TITLE OF INVENTION: THEM AND METHODS FOR WAKING AND USING THEM
CURRENT PAPLICATION NUMBER: US/10/370,370
CURRENT FLING DATE: 2003-2.18
PRIOR APPLICATION NUMBER: 60/357,406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Barton, Nelson R.
APPLICANT: Earton, Nelson R.
APPLICANT: Frey, Gerhard
TITLE OF INVENTION: CHIMERIC CANNULAE PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-115001
FILE REFERENCE: 09010-115001
CURRENT APPLICATION NUMBER: US/10/370,370
PRIOR APPLICATION NUMBER: 060/357,406
PRIOR FILING DATE: 2002-02-15
PRIOR FILING DATE: 2002-02-15
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 140
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                                                                                                                                                                                                                                                                                                                                                                                                      US-10-370-370-12
. Sequence 12, Application US/10370370
. Publication No. US20040006778A1
. GENERAL INFORMATION:
                                                                                                                                                 101 VISLDKPSAVIILD-EDFAI-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 EAKEGMLFDSLPVI 136
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Matches 119; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-370-370-12
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Matches
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                                                                                                                                                                                                                                                                                                                                          QLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTGY 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92 EQLKPYPKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTG 151
                                                                                                                                                                                                                                                                                    33 SFYATGTAQAVSEPIDVESHLG-SITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNA 91
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                                                                                                                                                                                                                                                             33 SFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAE 92
                                                                                                                                                                                                                        27; Gaps
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                                                                                                                                                                             29.5%; Score 307.5; DB 15; Length 131; 48.1%; Pred. No. 2.6e-24;
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jay Short
APPLICANT: Eric J. Mathur
APPLICANT: W. Michael Lafferty
APPLICANT: W. Michael Lafferty
APPLICANT: W. Michael Lafferty
APPLICANT: Netson Barton
TITLE OF INVENTION: Method of Making A Protein Polymer and
TITLE OF INVENTION: Mese of the Polymer
FILE REFERENCE: DOSE-1005US
CURRENT APPLICATION NUMBER: US/09/997,807
CURRENT FILING DATE: 2001-11-30
PRIOR FILING DATE: 2000-11-30
                                                                                                                                                                                                                        39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29.3%; Score 305.5; DB 10; Length ilarity 48.8%; Pred. No. 3.9e-24; Conservative 14; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       152 YINTSIWVPGEEDKIIVYNETKPVAILNFKAFYEAKEGML 191
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                                                                                                                                                                                                                                                                                                                                                                                                                    153 TNTSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGM 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                         -NNDIDNDGNND------AKIRVVAYYEAKEGM 131
                                                                                                                                                                                                                    16; Mismatches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 124
PRIOR FILING DATE: 2002-02-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-370-370-10
Sequence 10, Application US/10370370
Publication No. US2040006778A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 10, Application US/09997807; Publication No. US20030198681A1; GENERAL INFORMATION:
                                                                                                                   ORGANISM: Pyrodictium abyssi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Pyrodictium abyssi
                                                                                                                                                                                                                      76; Conservative
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Best Local Simi
Matches 78;
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                                                                                LENGTH: 131
                                                                                                                                      US-10-370-370-8
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                                                           SEQ ID NO 8
                                                                                                 TYPE: PRT
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                    Matches
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61 QLRPYFKYLIIKLVS-LDSN----GNBSEEKGMITLWKPYAVIILDHED------F 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92 EQLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTG 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 SFYATGTAEATSEPIDVVSNLNTAIAPAAGAQGSVGIGSITIENKTDVNVVKLKITLANA 60
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                      APPLICANT: O'Donoghue, Eileen
APPLICANT: Frey, Gerhard
TITLE OF INVENTION: CHIMERIC CANNULAE PROTEINS, NUCLEIC ACIDS ENCODING
TITLE OF INVENTION: THEM AND METHODS FOR MAKING AND USING THEM
FILE REFERENCE: 09010-115001
CURRENT APPLICATION NUMBER: US/10/370,370
CURRENT FILING DATE: 2003-02-18
PRIOR PELLING DATE: 2002-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 15; Length 124;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Eric J. Mathur
APPLICANT: W. Michael Lafferty
APPLICANT: Nelson Barton
APPLICANT: Revison Chow
TITLE OF INVENTION: Method of Making A Protein Polymer and
TITLE OF INVENTION: Uses of the Polymer
FILE REPERBNCE: DVSA-1005US
CURRENT APPLICATION NUMBER: US/09/997,807
PRIOR APPLICATION NUMBER: 60/250,426
PRIOR APPLICATION NUMBER: 60/250,426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 124
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20030198681A1
GENERAL INFORMATION:
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Best Local Similarity 47.2%
T5; Conservative
APPLICANT: Barton, Nelson R.
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nes 78; Conserv
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US-09-997-807-8
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                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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NUMBER OF SEQ ID NOS: 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 GTDYEKPVNEALTSVE-----KLKTSLRANPETVYDLNSIGSRVEALTDVIE--ALTFS 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 SGYETNSTALGN----FSETKAVISLDNPSAVI------VLDKEDIAVLYPDKTGYT 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 TLVAGALLFSPAVLEVHADQVTTPQVVNHVNSNNQAQQMAQKLDQDSIQLRNIKD--NVQ 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: S. agalactiae CAMP OTHER INFORMATION: factor
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                                                                                                                                                                                                            APPLICANT: PEREZ-CASAL, Jose
APPLICANT: PEREZ-CASAL, Jose
APPLICANT: FONTAIRE, Michael
APPLICANT: FONTAIRE, Michael
APPLICANT: SONTAIRE, MICHAEL
TITLE OF INVENTION: CAMP FACTOR OF STREPTOCOCCUS UBERIS
FILE REFERENCE: 9000-0030.20
CURRENT APPLICATION NUMBER: US/10/134,021
CURRENT FILIG DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
106 NND--IDGD-----NQCQ---IDATAYYEAKEGML 130
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182 RATIYTKSKLDKEI-WNTRFTRDKKVLNVKEF 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                154 NTSIWVPGEPDKIIVYNE--TKPVAILNFKAF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GSD---DIGYAIVWIKDQVNDVKLKVTLR----
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PUBLICATION NO. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
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PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
                                                                                                                                              Sequence 4, Application US/10134021
Publication No. US20030072765A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
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Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohlsen, Kari
Zyskind, Judith
Wall, Daniel
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Best Local Similarity
Matches 53; Conserva
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LENGTH: 255
                                                                                             RESULT 12
US-10-134-021-4
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APPLICANT:
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91 AEQLKPY-FKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVL---DKEDIAVLY 146
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PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PELICATION NUMBER: 60/230,335
PRIOR PLING DATE: 2000-09-06
PRIOR PLING DATE: 2000-09-06
PRIOR FILING DATE: 2000-09-09
PRIOR PLING DATE: 2000-10-29
PRIOR PLING DATE: 2000-10-29
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-11-27
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2000-12-22
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-12-27
PRIOR PLING DATE: 2001-02-09
PRIOR PLING DATE: 2010-10-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2010-10-0-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2010-10-0-09
PRIOR PLING DATE: 2010-10-0-09
PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR APPLICATION NUMBER: 60/269,308
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PRIOR PLING DATE: 2010-10-0-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2010-10-0-0-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR PLING DATE: 2010-10-0-0-09
PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PALM.
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Best Local Similarity 22.5%; Pred. No. 0.53;
Matches 38; Conservative 34; Mismatches 71; Indels 26; Gaps
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TITLE OF INVENTION: ANTIFUNGAL COMPOUNDS AND METHODS OF USE
FILE REFERENCE: 0342/10548-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/893,519A CURRENT FILING DATE: 2001-06-28
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APPLICANT: THOMPSON, Craig
APPLICANT: MOORE, Jeffrey
APPLICANT: BUURMAN, Ed T.
APPLICANT: BRADLEY, John
APPLICANT: DESILIVA, THAMARYA
APPLICANT: HARRIS, Sandra
APPLICANT: KOMARNITSKY, Svetlana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/215,164
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 60/224,457
PRIOR FILING DATE: 2000-08-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 34, Application US/09893519A Publication No. US20030027243A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , ORGANISM: Legionella pneumophila US-10-282-122A-61228
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MOORE, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MCCOY, Melissa
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ZHU, Shuhao
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fan
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APPLICANT: Stater, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERBNEE: 38-10(52052)8
FURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2003-02-28
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 1972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             159 SSTYSSVTLRQLSNPYYVNTIPEEDI-LKYVSYTLLATTSALFPFDHEQIQI-----PSK 212
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1 Similarity 24.1%; Pred. No. 8.5;
52; Conservative 38; Mismatches 81; Indels 45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

8.3%; Score 86.5; DB 10; Length 846;
Best Local Similarity 24.1%; Pred. No. 8.5;
Matches 52; Conservative 38; Mismatches 81; Indels 45.
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                                                                                                                                                                                                                                                                        ; NAME/KEY: misc feature
; OTHER INFORMATĪON: Corresponds to SEQ ID NO: 107
US-09-893-519A-34
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Publication No. US20030233675A1
GENERAL INFORMATION:
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
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                                                                                                                                                                                     ORGANISM: Saccharomyces cerevisiae
SOFTWARE: PatentIn version 3.1
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Best Local Similarity
Matches 52, Conserva
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US-10-369-493-1972
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US-10-369-493-1972
                                    SEQ ID NO 34
LENGTH: 846
                                                                                                                                                 TYPE: PRT
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213 IPNFESGLLHLIFEA--GLLYQSLGYKVEKFRMLNI 246
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В

Search completed: April 6, 2004, 12:39:46 Job time: 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

April 6, 2004, 12:37:42 ; Search time 20 Seconds (without alignments) 995.582 Million cell updates/sec Run on:

US-09-997-807-2 1042 1 VKYTFLAIAGIIASAAALAL......EGMLFDSLPVIFNFQVLQVG 207 Title: Perfect score: Sequence:

**2**83366 seqs, 96191526 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched:

Scoring table:

283366 Total number of Hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR 78:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description		1-acylglycerol-3-p	N-ethylammeline ch	hypothetical prote		extracellular prot	probable flagellin	exo-poly-alpha-gal	hypothetical prote	stomatin - mouse	conserved hypothet	hypothetical prote	ice nucleation pro	immunogenic protei	31K immunogenic pr	ABC-type transport	phage-related prot	probable PPE prote	ein			hypothetical prote	⊐	ice nucleation pro	auxin-induced prot	homoserine kinase	conserved hypothet			hypothetical prote
COLUMNIC	ID	1 0	7	9069	G72593	B83337	JC7306	A71169	\$72635	A90280	JC5221	F90167	S59262	JQ0188	IMBKBB	AF3351	S74812	B82552	B70625	VGBEEH	B46114	900695	E71086	MMHUND	S07053	S58494	D97052	G90254	D69008	A48421	B71426
	DB		7	~	7	N	7	7	Ŋ	(7	N	~	7	7	П	7	~	~	~	Н	~1	7	7	Н	~	~	7	~	7	7	~
	Length	1 0	707	427	533	174	449	334	1148	378	284	443	846	1258	329	329	223	739	391	468	458	870	4	1247	n	243	296	402	147	350	1942
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	Score		· '	91	16	06	σ,	•	œ,	88	ů.	86.5	ė.	86	85.5	ω,	84.5	4.	œ	83.5	e.		ω.	83	ω	ς.		ς.		82	
	Result No.		٠,	7	m	4	Ŋ	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

septum formation p	RGP1 protein - vea	probable methylmal	Fibrinogen-binding	hypothetical prote	probable peptidogl	hypothetical prote	HlyD family secret	hypothetical prote	hypothetical prote	glucose inhibited	hypothetical prote	fima protein - Dic	C4-dicarboxylate t	site-specific DNA-
C71873	S51865	A96023	AC1214	C72647	AB1180	876719	E87349	S77340	C70667	E90543	E90595	S15268	E83737	A64594
(1)	N 10	N	7	7	N	N	7	ď	N	N	N	~	~	7
493	663	712	862	1554	2044	253	388	433	494	611	099	161	341	598
7.8	0 6.	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.8	7.7	7.7	7.7
81.5	81.5	81.5	81.5	81.5	81.5	81	81	81	81	81	81	80.5	80.5	80.5
30	3 2	33	34	35	36	37	38	39	40	41	42	43	44	45

### ALIGNMENTS

RESULT	1
T22599	
1-acylg	1-acylglycerol-3-phosphate O-acyltransferase (BC 2.3.1.51) homolog F59F4.4 - Caenorhabd
C; Date:	c.pecines: caemoinadulis elegans C.Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 06-Oct-2000
C;Accession: P.Dobson P	C;Accession: T22599; T23012
submitt	submitted to the EMBL Data Library, October 1996
A;Reter A;Acces	A;Reference number: Z19587 A:Accession: T22599
A;Statu	A;Status: preliminary; translated from GB/EMBL/DDBJ
A; Resid	ninoscure ryke: una A.Residues: 1-262 «WIL>
A;Cross	A.Cross-references: EMBL:Z81089; PIDN:CAB03139.1; GSPDB:GN00028; CESP:F59F4.4
A; Experime	A;Experimental source: clone P53H4
submitt	nymental, v. submitted to the BMBL Data Library, October 1996
A;Refer	A;Reference number: Z19652
A; Accession:	ssion: T23012
A; Statu	A;Status: preliminary; translated from GB/EMBL/DUBU . MAJed: trae: DNN
A;Resid	A.Reddues: 1-262 kWI2>
A; Cross	A.Cross-references: EMBL:Z81095; PIDN:CAB03160.1; GSPDB:GN00028; CESP:F59F4.4
A; Experimen	imental source: clone F59F4
A; Gene:	/-enterlas- A:Gene: CESP:F59F4.4
A; Map p	A, Map position: X
A; Intro C; Super	A,Introns: 57/2; 102/1; 160/3; 192/3 C;Superfamily: mouse 1-acylglycerol-3-phosphate O-acyltransferase
C; Keywo	C;Keywords: acyltransferase; coenzyme A
Query	Query Match 9.2%; Score 95.5; DB 2; Length 262;
Matches	58; Conservative 2
δλ	4 TILAIAGIIASAAALALIAGFATTQSPLNSFYATG 38
οqα	
δ	39 TAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTL 88
qα	62 IFQAMTWEMGVRFELRNSEILHDKKPYIIIANHQSALDVLGMSFAMPVDCVVMLKSSL 119
δλ	89 RNAEQLKPYFKYLOIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPD 148
DÞ	120KYLPGFNLCAYLCDSVYINRFSKEKALKTVDTTLHEIVTKKRKVWI-YPE 168
δλ	149 KTGYTNTSIWVPGEPDKIIVYNETKPVALLNFKAFYEAKEGMLFDSLPVI 198
qq	169 GTRNAEPEL-LPPKKGAFILAKQAKIPIVPCVFSSHKPFYSHAEKRLTSGNCIIDILPEV 227

RESULT 2	DbTASAIVEVVEATITLDKSQVGVGFVLTAEVEGLGGG
N-ethylammeline chlorohydrolase homolog - Methanobacterium thermoautotrophicum (strain D	Qy 150 IGYTNTSIWVPGEPDKIIVYNETKPVAILNPKAF
C.Decession: GG-0007 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999 C.Accession: GG-0067	Db 169 SGRAVASFTVPPLPSGVHTVELVYTPPLWLRFQSI
R;Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Olu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. Y.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N. J. Bacteriol. 179, 7135-7155, 1997 A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MOID:98037514; PMID:9371463 A;Accession: G69067 A;Status: preliminary; nucleic acid sequence not shown, translation not shown	RESULT 4 B83337 hypothetical protein PA2464 [imported] - Pseudomonas C; Species: Pseudomonas aeruginosa C; Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #S; Stovesion: B83337 R; Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi,
A,Molecule type: DNA A,Residues: 1-427 <mth> A,Residues: 1-427 <mth> A,Residues: 1-427 <mth> A,Cross-references: GB.AE000910; GB.AE000666; NID:g2622610; PIDN:AAB85980.1; PID:g262262 A,Experimental source: strain Delta H C,Genetics: A,Genetics: A,</mth></mth></mth>	adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Fol. Jory, S., Olson, M.V. Nature 406, 959-964, 2000 A/Title: Complete genome sequence of Pseudomonas aer A/Reference number: A82950; MUID:20437337; PMID:1096
Query Match 8.7%; Score 91; DB 2; Length 427; Best Local Similarity 22.6%; Pred. No. 8.2; Matches 40; Conservative 29; Mismatches 80; Indels 28; Gaps 6;	Ablatus: preliminary Ablocule type: A;Residues: 1-174 <sto> A;Cross-references: GB:AE004674; GB:AE004091; NID:G' A;Experimental source: strain PAO1</sto>
Qy 22 AGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIK 76	CyGenetics: A/Gene: PA2464 A/Gene: PA2464 Guery Match Reat Incal Similarity 26.08: Dred MA 3 2.
Qy 77 DQVNDVKLKVTLRNAEQLKPYFKYLQIGITSGYETNSTALGNFSET 122	vative 27; LALLAGFATTQSF
QY 123 KAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKP 174  Db 313 KTASLLQKVNLEDPTALPAMDVFSMATLNGARALGIDAGLIAPGKLADIVILNTRRP 369	Db 3 ARIAALGILILPILAAGSAVAAEEGSSVKDAAKA-AVSSA Qy 60 AGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEG
F THERE	
G12593  hypothetical protein APE1216 - Aeropyrum pernix (strain K1)  C;Species: Aeropyrum pernix  C;Decies: Aeropyrum pernix  C;Decies: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999 C;Accession: G72593	Qy 116LGNFSETKAVISLDNPSAVIVLDKEDIAVLX      ::    ::    ::   Db 107 TVRLINLTQTGALLVIDNDGYSNALVALANPDDVTV
R; Kawarabayasi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Yamazaki, Y.; zaki, Yamazaki,	RESULT 5 JC7306 extracellular proteinase (EC 3.4.21) prtY - Lactob C;Species: Lactobacillus helveticus C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #
A,Status: preliminary A,Molecule type: DNA A,Rolecule type: DNA A,Residues: 1-533 «KAM» A,Residues: 1-533 «KAM» A,Residues: 1-533 «KAM» A,Residues: 1-533 «KAM» A,Residues: 1-532 «KAM» A,Residues: 1-532 «KAM» A,Residues: 1-532 «KAM» A,Residues: 1-532 «KAM» A,Residues: DDBJ.AP000061; NID:g5104821; PIDN:BAA80205.1; PID:d1043991; PID:g510 A,Experimental source: strain Kl A,Genetics: APR1216 A,Genetics: APR1216	Rivamento, N.; Shinoda, T.; Takano, T. Biosci. Biotechnol. Biochem. 64, 1217-1222, 2000 A;Title: Molecular cloning and sequence analysis of A;Reference number: JC7306 A;Accession: JC7306 A;Molecule type: DNA
Query Match  Query Match  Best Local Similarity 22.4%; Pred. No. 11;  Matches 49; Conservative 24; Mismatches 76; Indels 70; Gaps 9;	A;Cross_references: DDBJ.AB026985 A;Experimental source: strain CP790 C;Genetics:
Qy S TLAIAGIIASAAALALAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAGG 64	Ouery Match  Best Local Similarity 24.0%; Pred. No. 12;
Oy 65 SDDIGYAIWMIKDQVNDVKLKVTLRNAEQLKPYFKYLQ1QITSGYET 111  Db :     :     :     :      58YDVVEVMLSTGVSEVLIATLYLGSAGEGVELVGLPRSLEPGGVYTLEFRALSGL 110	MALCHES 52; CONSEIVALIVE 53; MISMALCHES 87  QY 11 IIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPID :
Qy 112 NSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDK 149	Db 8 VSAAAAALLAVAPVAATAMPVNAATTYTTSTTTNKFTV Qy 60AGAQGSDDIGYAIVWIKDQVNDVKLKVTI

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S.D., Warrener, P.; Hickey, M.J.; B
lger, K.R.; Kas, A.; Larbig, K.; Lim
                                                                                                                                                                                                                                                                                                                                                                   9948512; PIDN:AAG05852.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a gene encoding an extracellular pr
                                                                                                                                                                                                                                                                     ruginosa PA01, an opportunistic path
84043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Indels 38; Gaps 8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OLKPYFKYLQIQITSGYETNSTA 115
SGVSYAYQLRMGGVTVAVVYPDD 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LRNAEQLKPYF-----KYLQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIDV-ESHLGSIT-----PA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |: :: || ::
AIETGKNLLGGVSEGITSGRQSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ||:
|VDLSGAGSVSESKDTVNVTPSFT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DVESHLGS-----1TPA-- 59
                                                                                                                                         aeruginosa (strain PAO1)
                                                                                                                                                                         text_change 31-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | | | :: |
-PAKAGIRQTFVFEGG 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bacillus helveticus
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                                                          IY 204
                               Y 184
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9

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hypothetical protein SSO1258 [imported] - Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: Sulfolobus solfataricus C;Species: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001 C;Gracession: A90280 R. R.;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Char Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J. submitted to GenBank, April 2001 A;Description: Sulfolobus solfataricus complete genome.
                                                                                                                                                                                                                      Thermoanaerobacterium endo-1,4-beta-xylanase A; S-layer repeat homology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99 SAVEMALWSLKARKSNVELYKLİGDKIRDSVKVYASFPRFGKIDDVLIATRKSLERGFDL 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 LQIQITSGYETNSTALG-----NFSETKAVISLDNPSAVIVLDKEDIAVLYPDKT--- 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -- KVTLRNAEQLKPYFKY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-378 «KUR»
A;Cross-references: GB:AE006641; NID:g13814452; PIDN:AAK41496.1; GSPDB:GN00155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --ETNSTALGNF--SE 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 YSDITDYKITVSDSVYEQVYYASENQTVASQYIKQFYDNNVGDLKDDNGNTVMSAYKISM 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 TKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVAILNFK 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----NIINVE 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19 ALLAGFATTQSPLNSFYATGTAQAV----SEPIDVESHLGSITPAAG----AQGSD 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---DIGFILVWHKPDN 64
                                                                                                                                     A) Experimental Source: EMI
C) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Genetics:
A) Holose-binding repeat homology
C) Keywords: A) Hodrolase; polysaccharide degradation
C) Keywords: A) Hodrolase; polysaccharide degradation
F) 1-30 Domain: Signal sequence #status predicted <BIG>F) 1-30 Domain: S-layer repeat homology <SLR1>
F) 1028-1081 Domain: S-layer repeat homology <SLR1>
F) 1028-1081 Domain: S-layer repeat homology <SLR2>
F) 1092-1144 Domain: S-layer repeat homology <SLR3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 LLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIK-DQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 HSFVLTGLKPNTLYTIQVQSVDANKNTSTPVTITQSTAPSTPSE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14 LLAFLMVFTMPMSKAFADTTSSGPAAPVDLOVLSGSVT---
A;Reference number: S72621; MUID:97033555; PMID:8879252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 VNDV-KLKVTLRNAEQLKPYFKYLQIQITSGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

8.5%; Score 88.5;
Best Local Similarity 19.1%; Pred. No. 46
Matches 37; Conservative 38; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.4%; Score 88; 22.5%; Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    182 AFYEAKEGMLFDSL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 STGAVGDĠVĽAĎDV 188
                               A, Accession: S72621
A, Moleoule type: DNA
A, Residues: 729-1148 < MAW>
A, Cross-references: EMBL:US0951
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A;Residues: 1-334 <KAW>
A;Croser-references: GB-7000002, NID:g3236129; PIDN:BAA29638.1; PID:g3256955
A;Croser-references: strain OT3
A;Note: this accession replaces an interim accession for a sequence replaced by GenBank, C,Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: archaeal flagellin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---RVGNSANELYFLAELMQNLGATIKFDNGSVQV-YFDPTDWTSAA-----PTVIID 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           52 HLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYET 111
           68 LTSAAKGIPATLQGSIEASLNGTSVTADVAKDVTLTDGKGVAVYSYDKNTLTNKLSD 127
                                                                                          IQITSGYETNSTALGNFSETKA----VISLDNPSAVIV----LDKEDIAVLYPDKTGYTN 154
                                                                                                                                                 128 VKAGDDÝTMTLSGVG-FSFGKANAGKTLTFKLÞEGVTVEGANYNKDDHKVTL-DQYGNVS 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AGFATTQSPLNSFYAT---GTAQAVSEPIDVES 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63; Indels
                                                                                                                                                                                                                                                               186 GLKFV---ISKVKAYDSANTNAV----SFYDAKSGLV 215
                                                                                                                                                                                                           155 TSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML 191
                                                                                                                                                                                                                                                                                                                                                                                                        probable flagellin B precursor - Pyrococcus horikoshii
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C)Date: 08-Jul-1995 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000 C;Accession: S59262; S55157; $63067; S63071; S67329 R;Mailet, L.; Bussereau, F.; Jacquet, M. Asst II, 1195-1209, 1995 A;Title: A 43.5 kb segment of yeast chromosome XIV, which contains MFA2, MEP2, CAP/SRV2 A;Reference number: S59241; MUID:96109932; PMID:8619318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hypothetical protein YNL126w - yeast (Saccharomyces cerevisiae)
N,Alternate names: hypothetical protein JTA846; hypothetical protein N1222; hypothetica
C,Species: Saccharomyces cerevisiae
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A;Cross-references: EMBL:271402; NID:g1302059; PID:g1302060; MIPS:YNL126w
A;Cross-references: etrain S288C
A;Experimental source: strain S288C
A;Cantoni, A.; d'Angelo, M.; dal Pero, F.; Sartorello, F.; Pandolfo, D.; Lanfranchi, Skidhtted to the EMBL Data Library, February 1996
A;Description: The DNA sequence of cosmid 14-13b from chromosome XIV of Saccharomyces
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A,Cross-references: EMBL:Z46843; NID:g861113; PIDN:CAA86899.1; PID:g861114
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1994
                                                                                                                                                                                                                                                                                                                                                                                                                 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       145 GDRGIIGSIAGLGMSGDYTYELITYRKKENWLKKRMINKDSVKRVDESTFPLTFANYDYI 204
                                                                                                                                                                                                      -IQITSGYETNSTA----L 116
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-DOV 79
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A;Cross-references: EMBL:Z71402; NID:g1302059; PID:g1302060; MIPS:YNL126w
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C;Superfamily: Saccharomyces cerevisiae hypothetical protein YNL126w
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A; Residues: 1-730, 'S',732-846 <MAW>
A; Residues: BML: Z46848
A; Cross-references: EMBL: Z46848
R; De Antoni, A.; D Angelo, M.; Dal Pero, F.; Sartorello, submitted to the Protein Sequence Database, April 1996
A; Reference number: S63047
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R;Mallet, L.; Bussereau, F.; Jacquet, M.
submitted to the Protein Sequence Database, April 1996
A;Reference number: S63069
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A,Cross-references: SGD:S0005070; MIPS:YNL126w
     51 SHLGSITPAAGAQGSDDIGYAIV--
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C;Species: Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 12-Jun-2003
C;Accession: P90167
R;She, Q: Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Jong, I.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, Farrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
Submitted to GenBank, April 2001
A;Recence number: A99139
A;Recence number: A99139
A;Accession: F90167
A;Status: preliminary
A;Status: preliminary
A;Status: L-443 <cus conserved protein MJ095
C;Genetics: 1-443 <cus conserved protein MJ095
C;Superfamily: uncharacterized conserved protein MJ095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Appeciates: Mus musculus (house mouse)
C;Speciaes: Was musculus (house mouse)
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C;Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 24-Sep-1999
C;Schlegel, W.; Unfried, I.; Prohaska, R.
Gene 178, 115-118, 1996
A;Title: Cloning and analysis of a cDNA encoding the BALB/c murine erythrocyte band 7 in A;Recession: UC5221
A;Recession: UC5221
A;Recession: UC5221
A;Accession: UC5221
A;Acc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VONATLAVANITNADSATRLLA-----OTTLRN--ALGINNLSQILSDREEIAHHMOSTL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        58 PAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --MAAEAEAREARAKVIA 223
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 AEGEMNASRALKEASMVIT---ESPAAL---QLRYLQTLTTIAAEKNSTIVF 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: band 7 integral membrane protein; protein 7.2b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68; Indels
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26.2%; Pred. No. 11;
tive 28; Mismatches
                                                                --GYTNTSIWVPGEPDKIIVYNETKPVAI 177
                                                                                                                                     209 EIEWIEEPLWPPNDYDLLSKLTEFSPIPI 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52; Conservative
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Best Local Similarity
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Best Local Similarity
Matches 52; Conserv
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Query Match

Accession: JT0279  Mayfield, J.E.; Bricker, B.J.; Godfrey, H.; Crosby, R.M.; Knight, D.J.; H  10 63, 1-9, 1988  Title: The cloning, expression, and nucleotide sequence of a gene coding  Reference number: JT0279  Moccule type: mRNA  Moccule type: mRNA  Moccule: J-329 cMX'>  Cross-references: GB:M20404; NID:gl44104; PIDN:AAA22993.1; PID:gl44105  Comment: Brucella abortus is the causative agent for brucellosis in cattl  1-28/Domain: signal abortus fatatus predicted cSIG>  29-329/Product: immunogenic protein BCSP31 #status predicted cMAT>  Query Match  B.2%; Score 85.5; DB 1; Length 329;  Best Local Similarity 19:3%; Pred. No. 17;  Matches 56; Conservative 28; Mismatches 73; Indels 133; Gaps	QY 2 KYTTLATAGIIASAAALALLAGFATTOSPLNSYTATGTAQASEBIDVESHIGSITPAGG 61  bb 6 KIRRLAVAAVAGAIALGASFAVAQAPTFFRIGTGGTAGTYYPIGGLIANAISGAG 60  QY 62 AQG	RESULT 14 AP3351 31K immunogenic protein precursor [imported] - Brucella melitensis (strain 16M) C;Species: Brucella melitensis C;Species: Brucella melitensis C;Species: Brucella melitensis C;Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 15-Feb-2002 C;Accession: AF3351 R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; I.; Mazur, M.; Goltsman, E.; Selkov, E.; Blzer, P.H.; Hagius, S.; O'Callaghan, D.; Froc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002 A;Title: The genome sequence of the facultative intracellular pathogen Brucella A;Reference number: A3522; PMID:11756688 A;Accession: AF3351 A;Accession: AF3351 A;Accession: AF3352 A;Accession: AF3352 A;Accession: AF3353 A;Accessi	A;Gene: BME10796  A;Gene: BME10796  A;Map position: I C;Superfamily: immunogenic protein BCSP31  Query Match 8.2%; Score 85.5; DB 2; Length 329; Best Local Similarity 19.3%; Pred. No. 17; Matches 56; Conservative 28; Mismatches 73; Indels 133; Gaps 13; Qy 2 KYTTLAIAGIIASAAALALIAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAG 61
Best Local Similarity 24.1%;   Pred. No. 45;   Indels 45;   Gaps 12;   Matches 52;   Conservative 38;   Mismatches 81;   Indels 45;   Gaps 12;   Conservative 38;   Mismatches 81;   Indels 45;   Gaps 12;   Conservative 38;   Mismatches 80;   Mismatches 11;   M	RESULT 12 JOODS 8 ice nucleation protein - Erwinia herbicola C;Species: Erwinia herbico.a C;Species: Erwinia herbico.a C;Species: Erwinia herbico.a C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 26-Aug-1999 C;Accession: JOODS 8: 535273 R;Warren, G; Corotto, L. Gene 85, 239-242, 1989 A;Title: The consensus sequence of ice nucleation proteins from Erwinia herbicola, Pseud A;Reference number: JQ0188; MUID:90152370; PMID:2515997 A;Accession: JQ0188 A;Rolecule type: DNA A;Residues: 1-1258 *WAR> A;Cross-references: EMBL:M26382; NID:g148419; PIDN:AAA24823.1; PID:g148420 A;Experimental source: strain M1 R;Gurian-Sherman, D; Lindow, S.E.; Panopoulos, N.J. Mol. Microbiol: 9, 383-391, 1993 A;Title: Isolation and characterization of hydroxylamine-induced mutations in the Erwini	1412688  2; Length 1258;  65; Indels 60; Gaps  AT-GTAQAVSEPIDVESHLGSITPA   :	Db 730 AGADSSLIAGYGSTQTASYHSSLTAGYGSTQTAREQSVLTT 770.  QY 108 GYETNSTALGNFSETKAVISLDNBSAVIVLDKEDIAVLYPDKTGYTNTS 156

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tral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes J.S.A. 99, 443-448, 2002
is.A. 99, 443-448, 2002
ence of the facultative intracellular pathogen Brucella meliten is2; PMID:11756688
                                                         pression, and nucleotide sequence of a gene coding for an immun
79; MUID:88255848; PMID:3133283
r, B.J.; Godfrey, H.; Crosby, R.M.; Knight, D.J.; Halling, S.M.
                                                                                                                                                                                                                  20404; NID:gl44104; PIDN:AAA22993.1; PID:gl44105
tus is the causative agent for brucellosis in cattle and man.
ic protein BCSP31
quence #status predicted <SIG>
genic protein BCSP31 #status predicted <MAT>
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19.3%; Pred. No. 17;
ative 28; Mismatches 73; Indels 133; Gaps 13;
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19.3%; Pred. No. 17;
ative 28; Mismatches 73; Indels 133; Gaps 13;
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ST4812

M.Alternate names: protein sll1623 - Synechocystis sp. (strain PCC 6803)

M.Alternate names: protein sll1623

C,Species: Synechocystis sp.
C,Species: Synechocystis sp.
C,Species: Synechocystis sp.
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A,Status: nucleic acid sequence not shown; translation not shown
A,Status: nucleic acid sequence not shown; translation not shown
A,Status: nucleic acid sequence not shown; translation not shown
A,FResidues: 1-223 «KAN»
A,Cross-references: EMBL:D90909; GB:AB001339; NID:g1652844; PIDN:BAA17773.1; PID:d101856
A,Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C,Superfamily: unassigned ATP-binding; P-loop; transport protein
C,Keywords: ATP, nucleotide binding; P-loop; transport protein
F;22-202/Domain: ATP-binding cassette homology <ABC>
F;39-46/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73 VWIKDQVNDVKLKVTLRNAEQL------KPYFKYLQIQITSGYETNSTALGNFSETKA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 V--KEKLSPQEVQVRVGEALQAVNLAEMARRPIY----ALSGGQKQRIAIAGAIARHCS 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----EPDKIIV 168
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                                                                        ::| ||
118 LRLLATLYPETIHIVARKDANIKSVADLKGKRVSLDEPGSGTIVDARIVLEAYGLTEDDI 177
                                                                                                                                                                                                         ---YFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVI 135
                                                                                                                                                                                                                                                                            178 KAEHLKPGPAGERLKDGALDAYF-----FVGGYPTGAISELAISNGISLVPISGPEADK 231
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                                                                                                                                                                                                                                                                                                                                                                                                                   136 VLDK-----EDI--AVLYPDKTGYTNTSI---WVPG--EPDKIIVYNETK 173
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A;Reference number: S74322; MUID:97061201; PMID:8905231
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8.1%; Score 84.5; Di
Best Local Similarity 22.5%; Pred. No. 12;
Matches 42; Conservative 33; Mismatches
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82 VKLKVTLR-
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GenCore version 5.1.6
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OM protein - protein search, using sw model

6, 2004, 12:34:02 ; Search time 17 Seconds (without alignments) 634.031 Million cell updates/sec April Run on:

1042 1 VKYTTLAIAGIIASAAALAL......EGMLFDSLPVIFNFQVLQVG 207 US-09-997-807-2 Perfect score: Title:

Sequence:

Gapop 10.0 , Gapext 0.5 **BLOSUM62** Scoring table:

141681 seqs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Listing first 45 summaries Maximum Match 100% Post-processing: Minimum Match 0%

SwissProt\_42:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### SUMMARIES

		æ			SUMMARIES		
Result No.	Score	Query Match	Length	DB	ID	Description	otion
			-			100	
4 (	· (		707	4 1	FUCT	Q93841	
7	2/		427	H	YFOS_METTH	027549	methanobact
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4	86.5		284	H	STOM MOUSE	P54116	
ഗ	ů.		846	Н	SP98_YEAST	P53540	Bacc
9	98		1258	٦		P16239	-
7	'n.		329	Н	BCSP_BRUME	P12920	bruce11a
80	83.5		468	Н	VGLC HSVEB	P12889	equine he
σ	۳.		870.	Н	RPA1 METTH	027125	methanc
10	83		1247	Н	NIDO HUMAN	P14543	
11	83		1322	~1	ICEA_PANAN	P20469	panto
12	82.5	7.9	243	7	AXI7_ARATH	038825	arabidop
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14	ď		633	Т	GIA2_FUSNN	Q8ri88	
15	ď.	•	1122	Н	DSG2_MOUSE	055111	-
16	$\infty$		350	Н	OTC RANCA	P31326	rana
17	•	•	417	Н		Q8ey78	lepto
18	81.5		493	Н	FTSA_HELPJ	Q9zkm3	helicobacte
19	•	•	663	,-1		P16664	saccharomyc
20	•	•	712	Н	MUTB_RHIME	086028	
21	σ.	•	611	Н		Q98qv8	
22	80.5	•	161	Н		P27906	
23	Ö	•	2104	Н	1 1	014157	
24	80	•	196	Н	YB17_METJA	058517	
25	80	7.7	537	Н	CH61_COREF	Q8cy27	corynebacte
26	80	•	612	,	GIDA MYCPN	P75221	
27	æ	-	880	Н	LYTD BACSU	P39848	bacillus su
28	o,		158	-	FMAA BACNO	P02975	bacteroid
53	o,	7.6	538	-		P38946	
30	σ.	-	749	Н	VP4 ROTGA	004916	rotavi
31	79.5	•	1196	-1	~	P14629	
32	o,	7.6	1461	Н	NEO1 HUMAN	092859	homo s
33	ď.	7.6	43	Н	Y43R IRV6	P18305	chilo

30 x 90 2 4 4 8 6 4 3 5

0361FE6C9710593E CRC64;

109 PC 29638 MW;

262 AA;

POTENTIAL. POTENTIAL. POTENTIAL.

23 49

FRANSMEM SEQUENCE

TRANSMEM TRANSMEM

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Acyltransferase; Transmembrane

Q9jmb5 rattus norv P16480 bacillus th Q9jkv1 mus misculu P39099 escherichia Q9j502 fowlpox vir Q1778 caenorhabdi P40583 saccharomyc P40581 saccharomyc P6954 southambton Q64544 southambton Q66384 methanococc	F/3141 Synechocyst
ADRM RAT C4AA BACTI ADRM MOUSE BEGQ_ECOLI V233 FOWPV XTUS_CAEEL X1V9 YEAST YGHB YEAST YGHB YEAST RPA1_METITW POLM SOUV3	oii_sini3
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407 1180 4080 455 512 375 537 817 865 1788	404
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### ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBL_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harris B., Dobson R.; Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Converts lysophosphatidic acid (LPA) into phosphatidic acid by incorporating acyl molety at the 2 position (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      П
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
--- CATALYTIC ATTULTY: Acyl-CoA + 1-acyl-sn-glycerol 3-phosphate COA + 1,2-diacyl-sn-glycerol 3-phosphate.
--- PATHWAY: De novo phospholipid biosynthesis; second step.
--- SUBCELTULAR LOCATION: Integral membrane protein (Potential).
--- SIMILARITY: Belongs to the 1-acyl-sn-glycerol-3-phosphate acyltransferase family.
                            093841; 093783;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
28-FEB-2003 (Rel. 41, Last annocation update)
Putative 1-acyl-sn-glycerol-3-phosphate acyltransferase F59F4.4
(BC 2.3.1.51) (1-AGP acyltransferase) (1-AGPAT) (Lysophosphatidic acid acyltransferase) (LPAAT).
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TIGRFAMs; TIGR00530; AGP acyltrn; 1.
Hypothetical protein; Phospholipid biosynthesis; Transferase;
262 AA
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PIR; T22599; T22599.
Wormhep; FSP4.4; CB11552.
InnerPro; IPR002123; Acyltrnsferase.
InterPro; IPR004552; Acyltrn.
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EMBL; Z81089; CAB03160.1; JOINED.
EMBL; Z81089; CAB03139.1; -.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                   Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
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CAEEL
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SEQUENCE FROM N.A.
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Best Local
                                                                                                                                                                                                     058284;
                                                                                                                                                                                                                                                                               PH0549
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PYRHO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                              62 IFQAMTWPMGVRFELRNSEILHDKKPYIIIANHQSALDVLGMSFAWPVDCV--VMLKSSL 119
                                                                                                                                                                          RNAEQLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVIVLDKEDIAVLYPD 148
                                                                                                                                                                                                    ---KYLPGFNLCAYLCDSVYINRFSKEKALKTVDTTLHEIVTKKRKVWI-YPE 168
                                                                                                                                                                                                                                  KTGYTNTSIWVPGEPDKIIVYNETK----PVAILNFKAFYEAKE-----GMLFDSLPVI 198
                                                                                                                                                                                                                                                              GTRNAEPEL-LPFKKGAFILAKQAKIPIVPCVFSSHKFFYSHAEKRLTSGNCIIDILPEV 227
                                                          -LLAGFATT---QSPLNSFYATG 38
                                                                                    TFLAILFVIAVLLLLAQLPVIGFYIRAVYFGMCLIIGGFLGGLASIPFGKSPNNHFRMFK 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Hartison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwani N., Caruso A., Bash D., Safer H., Patwell D., Prabhakar S., McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M., Daniels C.J., Mao J.I., Rice P., Noelling J., Reeve J.N.; Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics."; J. Bacteriol. 179:7135-7155 (1997).
                                                                                                                  TAQAVSEPIDVESHLGS-----ITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTL
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Archaea, Euryarchaeota, Methanobacteria, Methanobacteriales,
9.2%; Score 95.5; DB 1; Length 262; 24.2%; Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8.7%; Score 91; DB 1; Length 427; 22.6%; Pred. No. 3.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     80; Indels
                              96; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46441 MW; 439527DD142182CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical protein; Hydrolase; Complete proteome SEQUENCE 427 AA; 46441 MW; 439527DD142182CD CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- SIMILARITY: Belongs to the ATZ/TRZ family.
                                                                                                                                                                                                                                                                                                                                                                 (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29; Mismatches
                                                                                                                                                                                                                                                                                                                                       427 AA
                              27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Methanobacteriaceae, Methanothermobacter.
NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005847; Pept_M38_regn.
Pfam; PF01979; Amidohydro_1; 1.
ProDom; PD000518; Urease; 1.
                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR006680; Amidohydro 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Delta H;
MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein MTH1505.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE000910; AAB85980.1;
                                                           4 TTLAIAGIIASAAALA-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40; Conservative
                              58; Conservative
                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                 15-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998
                                                                                                                                                                                                                                                                                                                                      YF05 METTH
                                                                                                                                                                                                                                                                                                                                                                                                16-OCT-2001
                                                                                                                  33
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                                                                                                                                                                                                                                    149
                                                                                                                                                                                                                                                                                                                                                                                                                             MTH1505
                              Matches
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22 AGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPA----AGAQGSDDIGYAIVWIK 76

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     end an email to license@18b-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 HLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYET 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    112 NSTALGNFSETKAVIS--LDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVY 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       109 ----RVGNSANBLYFLAELMQNLGATIKFDNGSVQV-YFDPTDWTSAA-----PTVIID 157
197 AALADKNDLMIHIHVSETENEVSE----VSRSHGMTPVEYLDEVGVLGPRTVAAHCVWLK 252
                                                                      77 DOVNDV----KLKVT-----LRNAEQLKPYFKYLQIQITSGYETNSTALGN----FSET 122
                                                                                                                                    253 DWEIDVLAERDVKVSHNPSSNWKLASGVSPVARLLORGVNVSLGTDGAASNNNLDMFOEM 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8 IAGIIASAAALALL------AGFATTQSPLNSFYAT---GTAQAVSEPIDVES 51
                                                                                                                                                                                                          123 KAV----ISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKP 174
                                                                                                                                                                                                                                                   Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Orsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kidoh Y., Yamazaki J., Kushida M., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3."; DNA Res. 5:55-76(1998).
-!- FUNCTION: Flagellin is the subunit protein which polymerizes to form the filaments of archaeal flagella (By similarity).
-!- SIMILARITY: Belongs to the archaeal flagellin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75 LAVYİTPNAĞSSĞ------IDLTKVRITLSDG-QKQALFKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9CEAAA6E07C92296 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR002774; Arch flagellin.
Pfam: PF01917; Arch flagellin; 1.
Tagellum; Multigene family; Complete proteome.
SEQUENCE 334 AA; 35438 MW; 9CEAAA6E07C92296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
31-CTT-2001 (Rel. 40, Last annotation update)
Probable flagellin PH0549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.5%; Score 88.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98344137; PubMed=9679194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AP000002; BAA29638.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    170 NETKPVAILN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrococcus horikoshii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A71169; A71169.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              qq
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158 TTNKVIEIVN 167

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS01270; BAND 7; 1.
Erythrocyte; Transmembrane; Phosphorylation; Lipoprotein; Palmitate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: Thought to regulate cation conductance. SUBCELLULAR LOCATION: EXPOSED ON THE CYTOPLASMIC SURFACE OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CYTOPLASMIC (POTENTIAL).
S-palmitoyl cysteine (By similarity).
S-palmitoyl cysteine (By similarity).
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIINE=96374834; PubMed=8786142; Gallagher P.G., Turetsky T., Mentzer W.C.; Gallagher P.G., Turetsky T., Mentzer W.C.; Genomic organization and 5'-flanking DNA sequence of the murine stomatin gene (Epp72). Genomics 34:410-412(1996).
                             SIOM_MOUSE STANDARD; PRT; 284 AA.
P54116; Q60744; Q62455;
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Erythrocyte band 7 integral membrane protein (Stomatin) (Protein 7.2b).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=97080556; PubMed=8921901; Schlegel W., Unfried I., Prohaska R.; "Cloning and analysis of a cDNA encoding the BALB/c murine erythrocyte band 7 integral membrane protein."; Gene 178:115-118(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallagher P.G., Romana M., Lieman J.H., Ward D.C.; Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: Belongs to the band 7 / mec-2 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Bone marrow;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               U17297; AAA75024.1; -.
U50999; AAB18857.1; ALT SEQ.
U50993; AAB18857.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U50994; AAB18857.1; JOINED.
U50995; AAB18857.1; JOINED.
U50996; AAB18857.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; US0997; AAB18857.1; JOINED.
EMBL; US0998; AAB18857.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:95403; Epb7.2.
InterPro; IPR001107; Band 7.
InterPro; IPR001972; Stomatin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; X91043; CAA62503.1; -.
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PRINTS; PR00721; STOMATIN.
                                                                                                                                                                                                                                                                            STOM OR EPB72 OR EPB7.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00244; PHB; 1.
                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [3]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN=BALB/c; TIS
                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U50993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIPID
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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                             STOM_MOUSE
RESULT
                                                                                     THE HAM BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN AND BEEN
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69
                                                                                                                                                                                                            58 PAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALG 117
                                                                                                                                                                                                                                                                       1 VKYTTLAIAGIIASAAALALLAGFATTQSPLNSFYATGT----AQAVSEPIDVESHLGSIT 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -i. FUNCTION: Involved in microtubule organization by the microtubule organizing centre, the spindle pole body (SPB). Probably part of the microtubule attachment site at the SPB.
-i. SUBUNIT: Interacts with TUB4 and SPC97.
-i. SUBCELLULAR LOCATION: Nuclear.
-i. SUBLITY: Belongs to the GCP family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Geissler S., Pereira G., Spang A., Knop M., Soues S., Kilmartin J.V., Schiebel E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The spindle pole body component Spo98p interacts with the gamma-tubulin-like Tub4p of Saccharomyces cerevisiae at the sites of microtubule attachment."; EMBO J. 15:3899-3911(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97245296; PubMed=9090055; de Autoni A., D'Angelo M., Dal Pero F., Sartorello F., Fandolfo D., Pallavicini A., Lanfranchi G., Valle G.; The Dallavicini A., Lanfranchi G., Valle G.; Sarcharomyces cerevisiae reveals an unusually high number of overlapping open reading frames.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mallet L., Bussereau F., Jacquet M.; Mich contains MFA2, M. 43.5 kb segment of yeast chromosome XIV, which contains MFA2, ME2, CAPSRV2, NAM9, FKB1/FPR1/RBP1, MOM22 and CPT1, predicts an adenosine deaminase gene and 14 new open reading frames."; Yeast 11:1195-1209(1995).
                                                                                                                                                                                                                                                                                                                  118 NFSETKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVY 169
                                                                                                                                                                                                                                                                                                                                                224 AEGEMNASRALKEASMVIT---ESPAAL---QLRYLQTLTIAAEKNSTIVF 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes,
Saccharomycetales, Saccharomycetaceae, Saccharomyces.
                                                                                                                                                          31;
                                                                                                                         Score 86.5; DB 1; Length 284; Pred. No. 4.5;
                                                                                                                                                          68; Indels
V -> A (IN REF. 2).

L -> F (IN REF. 2).

F -> L (IN REF. 2).

F -> L (IN REF. 2).

V -> I (IN REF. 1).

N -> H (IN REF. 1).

8E49276611ACB4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
29-pindle pole body component SPC98.
SPC98 OR YNL126W OR N1222 OR N1879.
                                                                                                                                                                                                                                                                                                                                                                                                                                846 AA
                                                                                                                                            ; Pred. No. 4.5;
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96324398; PubMed=8670895;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=96109932; PubMed=8619318;
                                                                                               31403 MW;
                                                                                                                             8.3%;
                                                                                                                                                              45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
 37
40
43
91
273
283
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43
91
273
283
284 AA;
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                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI TaxID=4932;
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the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NYRAKIVQKSSGLNMENLANHEHLLSPVRAPSIYTEASFENMDRFSERRSMVSSPNRYVP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----LDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159 SSTYSSVTLRQLSNPYYVNTIPBEDI-LKYVSYTLLATTSALFPFDHEQIQI----PSK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 ATTQSPLNSFYATGTAQAVSEPI---DVESHLGSITPAAGAQGSDD-IGYAIVWIKDQVN 80
the Swiss Institute of Bioinformatics and the EMBL outstation
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SUBCELLULAR LOCATION: Outer membrane.
DOMAIN: CONTAINS 126 IMPEREECT REPEATS OF A CONSENSUS OCTAPEFTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE MISCELLANBOUS: A STRERIMPOSED.
MISCELLANBOUS: A STRETURAL OF SUBJECT OF THAT OF ICE.
                                                                                                                           EMBL; 246843; CAA36899.1; -.
EMBL; 269382; CAA93378.1; -.
EMBL; 269382; CAA93378.1; -.
EMBL; 259262; S59262.
EMBL; 259262; S59262.
Germonline; 143132; -.
SGD; S0005070; SFC98.
GO; GO:0005822; C:inner plaque of spindle pole body; IDA.
GO; GO:0005824; C:outer plaque of spindle pole body; IDA.
GO; GO:0005200; F:structural constituent of cytoskeleton; IDI.
GO; GO:0007020; P:microtubule nucleation; IPI.
GO; GO:00071; P:microtubule assembly (sensu Saccharomyces); IMP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATQLGPLIDFYKLQSLDSPETTIMWHKIEKFLDAL---FGIQNTDDMVKYLSVFQSLLPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warren G.J., Corotto L.V., "The consensus sequence of ice nucleation proteins from Erwinia herbicola, Pseudomonas fluorescens and Pseudomonas syringae."; Gene 85:239-242(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 DVKLKVTLR----NAEQLKPYFKYLQ-IQITSGY-ETNSTALGNFSETKAVIS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.3%; Score 86.5; DB 1; Length 846;
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Pfam; PF04130; Spc97, Spc98; 1.

Microtubule; Nuclear protein.

SEQUENCE 846 AA; 98226 MW; 803048B05D5E5105 CRC64;
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01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=90152370; PubMed=2515997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ice nucleation protein.
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                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         824
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MEDLINE=20020109; PubMed=11756688;
DelVecchio v.G., Kapatral V., Redkar R.J., Patra G., Mujer C., Los T.,
Jablonski L., Laren N., D'Souza M., Bernal A., Mazur M., Goltsman E.,
Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J.,
The genome sequence of the facultative intracellular pathogen
Brucella melitensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 YTTLAIAGIIASAALALLAGFATTQSP-LNSFYAT--GTAQAVSEPIDVESHLGSITPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----GSTQTASYHSSLTAGYGSTQTAREQSVLTT
                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                         90;
SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Brucellaceae; Brucella.
NCBI_TaxID=29459, 235;
                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 1258;
                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60 AGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYL----
                                                                                                                                                                                                                                                                                                                                      590E8A130077FBD4 CRC64;
                                                                                                                                                                                                                                                                                                 ICE nucleation; Repeat; Outer membrane.
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01-0CT-1989 (Rel. 12, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
BCSP31 OR BMEI0796.
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 23.7%; Pred. .v.. - ...
Matches 47; Conservative 26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             329 AA.
                                                                                                                                                                                                                                                 Pfam; PF00818; Ice nucleation, 65.
PRINTS; PR00327; IČENUCLEATN.
PROSITE; PS00314; ICE NUCLEATION; 45.
                                                                                                                                                                                                  PIR; JO0188; JO0188.
HSSP; P06620; IINA.
InterPro; IPR000258; Ice_nucleatn.
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MEDLINE=88255848; PubMed=3133283;
                                                                                                                                                                                                                                                                                                                                      1258 AA; 125084 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157 IWVPGEPDKIIV-YNETK 173
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                                                                                                                                                                                  EMBL; M26382; AAA24823.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90 NAEQLKP------YFKYLQIQITSGYETNSTALGNFSETKAVISLDNPSAVI 135
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Mayfield J.E., Bricker B.J., Godfrey H., Crosby R.M., Knight D.J., Halling S.M., Balinsky D., Tabatabai L.B., "The cloning, expression, and nucleotide sequence of a gene coding for an immunogenic Brucella abortus protein.", Gene 63:1-91980].
-I-MISCELLANBOUS: BRUCELLA ABORTUS IS THE CAUSATIVE AGENT FOR BRUCELLOSIS IN CATTLE AND MAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136 VLDK-----EDI--AVLYPDKTGYTNTSI---WVPG--EPDKIIVYNETK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             232 ILEKYSFFSKDVVPAGAYKDVAETPTLAVAAQWVTSAKQPDDLI-YNITK 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73; Indels 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.2%; Score 85.5; DB 1; Length 329;
19.3%; Pred. No. 6.5;
tive 28; Mismatches 73; Indels 13:
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Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
"The DNA sequence of equine herpesvirus-1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Equine herpesvirus type 1 (strain Ab4p) (EHV-1), and Equine herpesvirus type 1 (strain Kentucky D) (EHV-1) Viruses; dSDM4 viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UGLC HSVEB STANDARD; PRT; 468 AA. P12889; P36321; 01-00T-1989 (Rel. 12, Last sequence update) 10-0CT-2003 (Rel. 12, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) GLycoprotein C precursor (Glycoprotein 13). GC OR GP13 OR 16.
                                                                                                                                                                                                                                                                                                                                         EMBL, AE009521, AAL51977.1; -. EMBL, M20404; AAA22993.1; -. PIR, AF3351, AF3351. PIR, AF3351. Signal; Complete proteome.
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Local Sim-
56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                               "Expression in recombinant vaccinia virus of the equine herpesvirus 1 gene encoding glycoprotein gpl3 and protection of immunized
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virology 193:910.923(1993).
-!- SIMILARITY: Belongs to the herpesviruses glycoprotein C family.
-!- SIMILARITY: Contains 2 immunoglobulin-like domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunoglobulin domain; Glycoprotein; Transmembrane; Signal; Repeat.
STRAIN-Kentucky D;
MEDLINE=88275055; PubMed=2455821;
Allen G.P., Coogle L.D.;
"Characterization of an equine herpesvirus type 1 gene encoding iglycoprotein (gpl3) with homology to herpes simplex virus glycoprotein C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                           MEDLINE-89382761; PubMed-2550665;
Guo P., Goebel S., Davis S., Perkus M.E., Languet B., Desmettre
Allen G., Paoletti E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=Kentucky D;
MEDLINE=93212524; PubMed=8384760;
Matsumura T., Smith K.H., O'Callaghan D.J.;
"DNA sequence and transcriptional analyses of the region of the equine herpesyirus type 1 Kentucky A strain genome encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86F67AFD15AF1C89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
GLYCOPROTEIN C.
POTENTIAL.
IG-LIKE 1.
IG-LIKE 1.
IG-LIKE 0.
N-LINKED (GLCNAC..)
N-LINKED (GLCNAC..)
N-LINKED (GLCNAC..)
N-LINKED (GLCNAC..)
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E -> K (IN REF. 4)
V -> A (IN REF. 4)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, L07272; AAA46078.1; --
EMBL, M86664; AA802451.1; --
EMBL, M19966; AAA46077.1; --
EMBL, M29234; AAA46085.1; --
EMBL, S57834; AAB25944.1; --
PIR, A28149; VGBEH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF02124; Marek A; 1.
PRINTS; PR00668; GLYCPROTEINC.
PROSITE; PS50835; IG LIKE; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50889 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001038; Gp13 EHV.
InterPro; IPR007110; Ig-like.
InterPro; IPR001654; Marek_A.
                                                                                                                                                                                                                                                                                                                                                                                                           lmals.";
Virol. 63:4189-4198(1989).
                                                                                                                                                                          Virol. 62:2850-2858(1988).
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4468
4451
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622
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2003
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1007
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Best Local Similarity
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                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=Kentucky D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        glycoprotein C.";
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                                                                                                                                                                                         DNTTNANG--TESTHSHETTITCTKSLISVPYYKSVDMNCT-----TSVGVNYSEYRL 106
                                                                                                                                                           125 VISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVAILNFKAFY 184
                                                                               DDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALG-NFSETKA 124
                                      22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J., Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K., Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Giu D., Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R., Jiwan N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S., Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N., "Complete genome sequence of Methanobacterium thermoautotrophicum deltaH: functional analysis and comparative genomics.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COFACTOR: Zinc. SUBUNIT: M.thermcautotrophicum RNA polymerase is composed of four
                                      -----STPATPTHTTPNLTTAHGA-GS
LAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    subunits: A',A', B' AND B''.
SIMILARITY: THE COMBINED A'+A" SUBUNITS CORRESPOND TO THE A
SUBUNITS OF EUKARYOTIC RNA POLYMERASES I, II AND III AND TO THE
EUBACTERIAL BETA' SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of DNA into RNA using the four ribonucleoside triphosphates as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA-directed RNA polymerase subunit A' (EC 2.7.7.6).
RPOAl OR MIH1051.
                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                          870 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Methanobacteriaceae; Methanothermobacter.
                                      10 VAVAYLICAGAILTYASGASASSSQ----
                                                                                                                                                                                                                                               185 EAKE----GMLFDSLP--VIFN 200
                                                                                                                                                                                                                                                                                     146 RKKSRRGGQLGVIPDRLPKRQLFN 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Methanobacterium thermoautotrophicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Interpro; IPR000722; RNA pol A.
Interpro; IPR007080; RNA pol Rpbl 1.
Interpro; IPR007086; RNA pol Rpbl 3.
Interpro; IPR007083; RNA pol Rpbl 4.
Interpro; IPR007081; RNA pol Rpbl 5.
Interpro; IPR00592; RNA pol Rpbl 5.
                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=98037514; PubMed=9371463;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE000876; AAB85542.1; -
                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                G69006; G69006.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=187420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=Delta H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substrates.
                                                                                                                                                                                                      107 EIYLN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              \{RNA\}(N)
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027125;
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102
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                                                                                                                                                                                                                                                                                                                                                                                                        -----KIIVYN 170
                                                                                                                                                                                                                                                                                                                                                                                                                                       327 NISINEVGVPEIIAREVTVPVYVTEWNIDRMREYIENGPDVHPGANYVIRPDGRKIRIYN 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olsen D.R., Nagayoshi T., Fazio M., Mattei M.-G., Passage E., Weil D., Timpl R., Chu M.L., Uitto J.; "Human nidogen: cDNA cloning, cellular expression, and mapping of the
                                                                                                                                                                                                                                                                                         46 PIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLR-NAEQL--KPYFKYLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nagayoshi T., Samborn D., Hickok N.J., Olsen D.R., Fazio M.J., Chu M.-L., Knowlton R., Mann K., Deutzmann R., Timpl R., Uitto J.; "Human nidogen: complete amino acid sequence and structural domains deduced from CDNAs, and evidence for polymorphism of the gene."; DNA 8:581-594(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96044428; PubMed=7557988;
Zimmermann K., Hoischen S., Hafner M., Nischt R.;
"Genomic sequences and structural organization of the human nidogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene to chromosome 1943.";
Am. J. Hum. Genet. 44:876-885(1989).
-!- FUNCTION: Sulfated glycoprotein which is widely distributed in basement membranes and that is tightly associated with laminin. Also binds to collegen IV. It probably has a role in cellextracellular matrix interactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                             61;
                                                                                                        Transferase; DNA-directed RNA polymerase; Transcription; Zinc;
                                                                                                                                                                                          8.0%; Score 83.5; DB 1; Length 870; 21.7%; Pred. No. 31; ive 32; Mismatches 73; Indels 61
                                                                                                                                                           05BB2C2C80CFD211 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                      -ISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPD---
                                                                                                                                          C4-TYPE (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETKPVAILNFKAFYEAKEGMLFDSLPVIFNFQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P14543; Q14942;
01-GMN-1990 (Rel. 13, Created)
01-GMN-1990 (Rel. 13, Last sequence update)
01-MRA-2004 (Rel. 43, Last annotation update)
Nidogen precursor (Entactin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT; 1247 AA.
Pfam; PF04997; RNA POL RPbl 1; 1.
Pfam; PF00623; RNA POL Rpbl 2; 1.
Pfam; PF04983; RNA POL Rpbl 3; 1.
Pfam; PF05000; RNA POL Rpbl 4; 1.
Pfam; PF04999; RNA POL Rpbl 4; 1.
SMART; SM00663; RPOLA N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Placenta; MEDLINE=89270475; PubMed=2471408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90091745; PubMed=2574658;
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                                                                                                                        Complete proteome; Zinc-finger
ZN FING 60 103 C
                                                                                                                                                           870 AA; 98077 MW;
                                                                                                                                                                                                                                                                                                                                      103 IQITSGYETNSTALG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genomics 27:245-250(1995).
                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                171
                                                                                                                                                                                             Query Match
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PROSITE; PS00102; EGF 1; 1.
PROSITE; PS01186; EGF 2; 5.
PROSITE; PS01187; EGF 2; 5.
PROSITE; PS00187; EGF 2; 5.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
PROSITE; PS00484; THYROGLOBULIN_1; 1.
Signal; Calcium-binding; Repeat; EGF-like domain; Call adhesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I (LARGER GLOBULAR DOMAIN).
III (CYSTEINE-RICH).
IIII (SMALLER GLOBULAR DOMAIN).
EGF-LIKE 1.
EGF-LIKE 2.
                                                                                                                                                                                        domain.
-:- SUBUNIT: Interacts with FBLN1 (By similarity).
-:- SUBCELLULAR LOCATION: Basement membranes.
-:- PIM: N- and O-glycosylated.
-:- SIMILARITY: Contains 6 EGF-like domains.
-:- SIMILARITY: Contains 1 thyroglobulin type-I domair.
-:- SIMILARITY: Contains 5 LDL-receptor YWTD domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MILM, 1513-01; Asx hydroxyl_S.
InterPro; IPR00152; Asx hydroxyl_S.
InterPro; IPR001681; EGF_Ca.
InterPro; IPR006029; EGF_like.
InterPro; IPR006019; GFP_like.
InterPro; IPR009017; GFP_like.
InterPro; IPR009013; Idl receptor_rep.
InterPro; IPR000186; Nidogen_ext.
InterPro; IPR000186; Nidogen_ext.
InterPro; IPR000186; Thyroglobulin_1.
Pfam; PF00008; EGF; 6.
Pfam; PF00008; EGF; 6.
Pfam; PF00008; EGF; 6.
Pfam; PF000199; EGF_CA; 2.
SWART; SW00119; EGF_CA; 2.
SWART; SW00139; IV; 5.
SWART; SW00135; IV; 5.
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CAA57709.1; JOINED.
CAA57709.1; JOINED.
CAA57709.1; JOINED.
CAA57709.1; JOINED.
CAA57709.1; JOINED.
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X84836; CAA57709.1; JOINED.
X84837; CAA57709.1; JOINED.
M27445; AAA57261.1; -
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EMBL; X84835; CAA57709.1;
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Genew, HGNC:7821, NID.
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SEQUENCE FROM N.A.
MEDLINE=9009244; PubMed=2599095;
Abe K., Watabe S., Emori Y., Watanabe M., Arai S.;
Ah K., Watebe S., Emori Y., Watanabe M., Arai S.;
"An ice nucleation active gene of Erwinia ananas. Sequence similarity
to those of Pseudomonas species and regions required for ice
EGF-LIKE 3, CALCIUM-BINDING (POTENTIAL).
BGF-LIKE 4.
EGF-LIKE 5.
THYROGLOBULIN TYPE-I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 8.0%; Score 83; DB 1; Length 1247;
Best Local Similarity 23.7%; Pred. No. 52;
Matches 47; Conservative 23; Mismatches 72; Indels 56; Gaps
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Pantoea.
                                                                               LDL-RECEPTOR YWTD MOTIF 1.
LDL-RECEPTOR YWTD MOTIF 2.
LDL-RECEPTOR YWTD MOTIF 3.
LDL-RECEPTOR YWTD MOTIF 4.
EGF-LIKE 6.
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01-FEB-1991 (Rel. 17, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---QIQITS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GYETNSTA-----LGNFSETK----AVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTS 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 YTTLAIAGIIASAAALALLAGFATTQSP-LNSFYAT--GTAQAVSEPIDVESHLGSITPA
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids,
eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Auxin-responsive protein IAA7 (Indoleacetic acid-induced protein 7).
1AA7 OR AT3223050 OR MXC7.8.
Arabidopsis thaliana (Mouse-ear cress).
                                                                   enable bacteria to nucleate
                                                     -!- FUNCTION: Ice nucleation proteins enable bacteria to nucleat crystallization in supercooled water.
-!- SUBCELDUIAR LOCATION: Outer membrane (By similarity).
-!- DOMAIN: CONTAINS MANY IMPERPET REPEATS OF THE CONSENSUS OCTAPEPTIDE A-G-Y-G-S-T-X-T; FURTHER ON A 16-RESIDUE AND A REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
-!- SIMILARITY: Belongs to the bacterial ice nucleation protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=cv. Columbia,
MEDLINE=95387393; PubMed=7658471;
Abel S., Nguyen M.D., Theologis A.;
"The PS-IAA4/5-like family of early auxin-inducible mRNAs in
Arabidopsis thaliana..;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 83; DB 1; Length 1322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OCTAPEPTIDE PERIODICITY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. 56;
27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ice nucleation; Repeat; Outer membrane.
COMAIN 162 1281 OCTAPEPTID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro, IPR000258; Ice_nucleatn.
Pfam, PF00818; Ice_nucleation; 69.
PRINTS; PR00327; ICENUCLEATN.
PROSITE; PS00314; ICE_NUCLEATION; 49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 157 IWVPGEPDKIIV-YNETK 173
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                                   258:297-300(1989).
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22954850; PubMed=14593172;

MEDLINE=22954850; PubMed=14593172;

MEDLINE=22954850; PubMed=14593172;

MEDLINE=22954850; PubMed=14593172;

MEDLINE=22954850; PubMed=14593172;

MARAIDAN, Wu H.C., Kim C.J., Nguyen M., Pham P.K., Cheuk R.F.,

MARAIDAN, Quach H.L., Tripp M., Chang C.H., Lee J.M., Toriumi M.J.,

A rakawa T., Banh J., Banno F., Bowser L., Brooks S.Y., Carninci P.,

Chao Q., Choy N., Enju A., Goldsmith A.D., Gurjal M., Hansen N.F.,

Rhan S., Koesema E., Ishida J., Jiang P.X., Jones T., Kawai J.,

Kaniya A., Meyers C., Nakajima M., Narusaka M., Sakurai T.,

Satou M., Tamse R., Vayberg M., Wallender E.K., Wong C., Yamamura Y.,

Yuan S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;

"Empirical analysis of transcriptional activity in the Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NFSETKA-----VISLDNPSAVIVLDKEDIAVL--YPDKTG-----YTNTSIWVPGEPDK 165
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72
                                                                                                                                                                            Nakamura Y.;
"Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence
features of the regions of 4,504,864 bp covered by sixty Pl and TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13 ASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- FUNCTION: Could act as regulator of genes responsible for mediating the various auxin-induced events responsible for cell
                                                                                                                      Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 243;
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--- SUBCELLULAR LOCATION: Nuclear (By similarity).
--- INDUCTION: By auxin.
--- SIMILARITY: Belongs to the AUX/IAA family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDFMNESKLMNLINSSEYVPSYEDKDGDWMLVGDVP 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.9%; Score 82.5;
25.0%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73 VWIKDQVNDVKLKVTLRNAEQ-----
                                                             STRAIN=cv. Columbia;
MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AB026655; BAB02096.1; -. EMBL; AF332395; AAG48759.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U18409; AAC49048.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Science 302:842-846(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         54; Conservative
                                                                                                                                                                                                                                                                             clones.";
DNA Res. 7:131-135(2000).
                                                                                                                                                                                                                                                                                                                                       [3]
SEQUENCE FROM N.A.
THATALECY. COlumbia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S58494; S58494.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                        Nakamura Y
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- TGYTNT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | :: : | :: | :: | 35 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 135 | 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    190 LFNISRCSMLVSALNNG-----ENEKLRYLFEDKIHQPYRKKLINNIDSIFLKAKEYGSL 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ATCC 824 / DSM 792 / VKM B-1787;

MEDLINE-21359325; PubMed=11466286;

Meolling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,

Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,

Bennett G.N., Koonin E.V., Smith D.R.;

"Genome sequence and comparative analysis of the solvent-producing
bacterium Clostridium acetobitylicum.";

J. Bacteriol. 183:4623-4838(2001).

-! CATALYIIC ACTIVITY: ATP + L-homoserine = ADP + O-phospho-L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86; Indels 47; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- PATHWAY: Threonine biosynthesis from asparate; fourth step. -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential). -!- SIMILARITY: Belongs to the GHMP kinase family. Homoserine kinase
                                                                                                                                                                                                                                                                                                             Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 296;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TIGRFAMS, TIGRO0191, thrB, 1.
PROSITE; PS00627; GHMP KINASES ATP, 1.
Threonine blosynthesis; Transferase; Kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 ATP (POTENTIAL).
33072 MW; 809830C84B851346 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     156 SIWVPGEPDKII-VYNETKPVAILNFKAFYEA-KEG 189
                                                                                                28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Homoserine kinase (EC 2.7.1.39) (HK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    116 LGNFSETKAVISLDNPSAVIVLDKEDIAVLYPDK
                                       296 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 10;
38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7.9%; Score 82.5; 20.8%; Pred. No. 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
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HAMAP; MC_00384; -; 1.
InterPro; IPR006204; GHMP. kinase.
InterPro; IPR006203; GHMPKnse_ATP.
InterPro; IPR008970; Homoser_Kin.
Pfam; PP00288; GHMP_kinases; 1.
PRINTS; PR00958; HOMSERKINASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE007636; AAK79207.1; -.
                                                                                                                                                                                                                                                                                Clostridium acetobutylicum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45; Conservative
                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE 296 AA;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=1488;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        homoserine.
                                                                                                                                                                                                                                             THRB OR CAC1235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subfamily.
                                                                                                                                                                                                                                                                                                                                                     Clostridium
                                   CLOAB
                                                                                                                                                                                                                                                                                                                    Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                356 BIKYTLESRTVENL---FLAGOINGTSGYE-BAGAOGLMAGINAVRKLRNEEPVI-LDRA 410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 GFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIKDQVNDV 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 KLKVTL--RNAEQLKPYFKYLQIQITSGYBTNSTALGNFSETKAVISLDNPSAVIVLDKE
                                                                                                                                                                                                                                                                                                                                                                                       Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A., Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., Fonstein M., Kyrpides N., Overbeek R.; "Genome sequence and analysis of the oral bacterium Fusobacterium nucleatum strain ATCC 2586.";
J. Bacteriol. 184:2005-2018(2002).
-!- FUNCTION: Not known.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ch 7.9%; Score 82.5; DB 1; Length 633; l Similarity 26.8%; Pred. No. 25; 44; Conservative 22; Mismatches 67; Indels 33
                                                                                                                                                                                                                                       Fusobacterium nucleatum (subsp. nucleatum).
Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 D-----SYIGTLI-----DDLVSKGTNEPYRMFTARSEY 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 DIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVAILNFKAFY 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                633 AA; 71317 MW; 2EC1E8EFA5BF3B04 CRC64;
245 GEFISGSGSTLIAVLEEADENFILKWKTYLDSLKDG 280
                                                                                                                                            28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Glucose inhibited division protein A 2.
GlDA2 OR FN1723.
                                                                                                           633 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
ProDom; PD003738; GIDA; 1.
TIGREAM; TIGRO0136; gidA; 1.
PROSITE; PS01280; GIDA 1; FALSE_NEG.
PROSITE; PS01281; GIDA 2; 1.
Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HAMAP; MF_00129; ; 1.
InterPro; IPR001327; FAD_pyr_redox.
InterPro; IPR001218; GIDA.
InterPro; IPR004416; GidA_sub.
InterPro; IPR001016; NAD_BS.
InterPro; IPR001010; Pyr_redox.
Pfam; PP01134; GIDA; 1.
                                                                                                                                                                                                                                                                                                                                                        STRAIN=AICC 25586;
MEDLINE=21886394; PubMed=11889109;
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                                                                                                            STANDARD;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                NCB1_TaxID=76856;
                                                                                                                                                                                                                                                                                Fusobacterium.
                                                                                                            FUSNN
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                                                                                                                            QBRIBB;
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                                                                         RESULT 14
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STRAIN-C57BL/6J; TISSUE-Mammary gland;

MEDLINE-238257; PubMed-12477932;

MEDLINE-238257; PubMed-12477932;

MEDLINE-238257; PubMed-12477932;

MEDLINE-238257; PubMed-12477932;

MAISCHUL R., Feingold E.A., Grouse L.H., Derge J.G.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moorer T., Mang J., Hsieh F.,

Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Vödin T.B., Toshiyuki S., Carminci P., Prange C.,

Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Rutterfield Y.S.N., Krzywinski M.I., Schaks U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

Ruterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

"Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1042-1122 FROM N.A., AND TISSUE SPECIFICITY.

MEDLINE=98067789; PubMed=9404003;

King I.A., Angst B.D., Hunt D.M., Kruger M., Arnemann J., Buxton R.S.;

"Hierarchical expression of desmosomal cadherins during stratified epithelial morphogenesis in the mouse.";

Differentiation 62:83-96(1997).

-! FUNCTION: Component of intercellular desmosome junctions. Involved in the interaction of judgue proteins and intermediate filaments mediating cell-cell adhesion.

-! SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

-! TISSUE SPECIFICITY: Expressed uniformly in all B12.5 epithelia, gradually becoming confined to the basal cell layers during epithelial stratification.
                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN: Calcium may be bound by the cadherin-like repeats (Potential).
                                                                                                                                                                                                                                                                                                                                Zhuxiang N., Garrod D.R.; "Desmosomal cadherins mediate homophilic cell adhesion."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DSG2 MOUSE
OS5111; Q8K069; Q8R517;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
... Arr-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: Contains 4 cadherin domains.
                                                                                                                                                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                               TISSUE=Pancreas;
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EMBL; AB072269; BAB86843.1; -. EMBL; BC034056; AAH34056.1; -. EMBL; AJ000328; CAA03995.1; -.

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68 IGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNS-TALGNFS----- 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               263 VOIRILDUNDNIPVVENKMYEGTVEENQVNVEVMRIKVTDAYEVGSDNWLANFTFASGNE 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      207 SOEPANSHMFYLINKDTGEIYTTSFTLDREEHSSYSLTVEARDGNGOITDKPVOOAQ---- 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 -----ET-----KAVISLDNPSAVIVLDKEDIAVLYPDKTG------YTNTSIWVPG 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 TOSPLNS--FYA---TGTAQAVSEPIDVESHL------GSIT--PAAGAQGSDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   323 GGYFHIETDTQTNEGIVTLVKEVDYEEMKKLDLSIIVTNKAAFHKSILSKYKATPI----
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                                             PRINTS; FAVOURY CA, 4. SMARTY, SMOOLIZ; CA, 4. SMARTY, SMOOLIZ; CADHERIN 1; 3. PROSITE; PS50268; CADHERIN 2; 4. Cell adhesion; Glycoprotein; Transmembrane; Repeat; Signal; Calcium-binding.
                                                                                                                                                                                                                                                                                                                                                             58 I -> L (IN REF. 2).

80 E -> D (IN REF. 2).

91 V -> I (IN REF. 2).

63 T -> R (IN REF. 2).

122397 MW; CEC0C489F8SBED57 CRC64;
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                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
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CADHERIN 4.
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       GO; GO:0030057; C:desmosome; ID
InterPro; IPR001126; Cadherin.
Pfam; PF00028; cadherin; 4.
PRINIS; PR00205; CADHERIN.
MGI:1196466; DBg2.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

April 6, 2004, 12:37:17; Search time 45 Seconds (without alignments) 1451.384 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-997-807-2 1042 1 VKYTTLAIAGIIASAAALAL.......EGMLFDSLPVIFNFQVLQVG 207

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

1017041 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL 25:\*

1: sp\_archea:\*
2: sp\_bacteria:\*
4: sp\_bungi:\*
5: sp\_invertebrate:\*
6: sp\_mammal:\*
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sp\_archeap:\*

		Description	Q7v5v8 prochloroco	Q53651 streptococc	Q8vw91 lactobacill	Q80n15 yellow head	Q91cd3 ochrobactru	Q8cx23 streptococc	Q8cx01 streptococc	Q9ycp2 aeropyrum p	Q8av58 gallus gall	Q9i118 pseudomonas	Q9c2c4 neurospora	Q7wyn3 acetivibrio	Q9s0w9 lactobacill	Q8vw92 lactobacill	Q60045 thermoanaer	Q97yr3 sulfolobus
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	* 5	Match	9.6	9.2	9.1	0.6	8.8	8.7	8.7	8.7	8.7	8.6	9.8	8.6	9.8	8.6	8.5	8.4
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## ALIGNMENTS

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RESULT 1 2075V8 2075V8 AC Q7V5V8 AC Q7V5VB, DT 01-OCT-2003 (TEBMBLrel. 25, Created) DT 01-OCT-2003 (TEBMBLrel. 25, Last sequence update) DT 01-OCT-2003 (TEBMBLrel. 25, Last sequence update) DT 01-OCT-2003 (TEBMBLrel. 25, Last annotation update) DE Putative D-3-phosphoglycerate dehydrogenase (PGDH) (EC 1.1.1.95).	Prochlorococcus marinus (strain MIT 9313).  Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcacea; Prochlorococcus.  NCBI_TAXID=74547; [1]  SEQUENCE FROM N. A.  MEDLINE=22825699; PubMed=12917642;  Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Ahlgren N.A., Arellano A., Coleman M., Hauser L., Hess W.R., Shaw S.L., Steglich C., Sullivan M.B., Ting C.S., Tolonen A., Shaw S.L., Zinser E.R., Chisholm S.W.;  "Genome divergence in two Prochlorococcus ecotypes reflects oceanic niche differentiation.";  Nature 424:042:1047(2003).	EMBL; BX572099; CAE21606.1; Oxidoreductase; Complete proteome. SEQUENCE 532 AA; 56591 MW; 631E7E696500DA44 CRC64; Query Match Best Local Similarity 25.4%; Pred. No. 4; Matches 46; Conservative 28; Mismatches 71; Indels 36; Gaps	9 AGIIASAALALLAGFATTOSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDI 66
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                   118 NFSETKAVIS---LDNPSAVIVLD--KEDIAVLYPDKTGYTNTSIWVPGEPDKII-VYNE 171
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Lactobacillus.
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Med. Microbiol. Immunol. 183:239-256(1994).
EMBL, X72754; CAA51283.1; -.
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255 PO
28373 MW;
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Best Local Similarity 25.0*
--heq 53, Conservative
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                                                                                                                                                                                                                                                                                                                                                                      Streptococcus agalactiae.
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                                                                                                                                                                                                                                                                                                                                                   CAMP factor precursor
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                                                                                                                                             410 T 410
                                                                                                       172 T 172
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=R268;
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961 HSVTCINSKDNKVHVVKQPGY---SYXIAGDPGALHISHNKHKPYTSILKDQINLFHFSY 1017
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 Q-----VNDVKLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNFSETKAVISLDNP 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKI-LVYNETKP-----VAILNFKA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 LTSAAKGIPÄTLÖGSIEASLNGTSVTADVADVAKDVTLKD-DGGKTVYSYNEGEKKVDNN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105 ---ITSGYETNSTALG-NFSETKA----VISLDNPSAVIVLD-KEDIAVLYPDKTGYTNT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 LSAVEAGKEYTMÍLSGVGFSFGKÁNAGKTLTFKLÞKNÝKVNDÍTSNÓVKVSLDQYGNAÍNL 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 919 NGPYSLGVPDVSCEI---HDETL------TCG--TNSTF--RFSICSHKIPYDGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----ITPA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 -----AGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNAEQLKPYFKYLQIQ-----
Saito Y., Hamanaka Y., Takizawa S., Benno Y.; ^{\prime} "Rapid Detection of Lactobacillus helveticus in Fecal Samples of Healthy Subjects Administered L. helveticus Yogurt using S-layer Gene-
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EMBL; AFS40644; AAO83987.1; SEQUENCE 1666 AA; 185430 MW; COB523A754D6EA9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               no DNA stage; Nidovirales.
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                                                                                      Targeted Primers.";
Targeted Primers.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AB061776; BAB72066.1; -
GO; GO:0009274; C:cell wall (sensu Bacteria); IEA.
GO; GO:00030115; C:S-Layer; IEA.
GO; GO:0005199; F:structural constituent of cell wall; IEA.
InterPro; IPR004903; SLAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71; Indels
                                                                                                                                                                                                                                                                                                                                                                                       9.1%; Score 95; DB 2; Length 449; 24.9%; Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 IIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGS----
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                                                                                                                                                                                                                                                                                                                                      449 AA; 47940 MW; EBA76530777D343A CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       156 SIWVPGEPDKIIVYN-ETKPVAILNFKAFYEAKEGML 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                86;
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95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, NCBI_TaxID=96029;
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01-JUN-2003 (TrEMBLrel. 24, Last sequ
01-JUN-2003 (TrEMBLrel. 24, Last anno
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SEQUENCE FROM N.A.
MEDLINE=22541857; PubMed=12655087;
                                                                                                                                                                                                                                                                                     Pfam; PF03217; SLAP; 1.
PRINTS; PR01729; SURFACELAYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      54; Conservative
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Best Local Similarity
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CFB OR SAG2043.
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                                                                                Query Match
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Q8CX01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98 FSTGT-----PVTVDDVIFSLQKAADPQGS--FGFAFEPIKSIDKIDDKTVRLTLKH-- 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=2224268; PubMed=12354221;
Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
Msadek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
Kunst F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 YAŢGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIK--DQVNDVKLKVTLRNAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                  47; Indels 35; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of Streptococcus agalactiae, a pathogen causing
                                                                                                                                                                                                                                                   MEDILINE-20193677, PubMed-10727942, Komeda H., Assano Y., Romeda H., Assano Y., "Gene cloning, nucleotide sequencing, and purification and characterization of the D-stereospecific amino-acid amidase from
                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 508;
                                                                                                                                                                     Ochrobactrum anthropi.
Bacteria, Proteobacteria, Alphaproteobacteria, Rhizobiales,
Brucellaceae, Ochrobactrum.
NCBL_TaxID=529,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus agalactiae (serotype III).
Bacteria, Firmicutes, Lactobacillales, Streptococcaceae,
                                                                                                                                                                                                                                                                                                                          EMBL; AB026907; BAA94699.1; -.

GO; GO:0005215; F:transporter activity; IEA.

GO; GO:000610; P:transporter activity; IEA.

InterPro; IPR000914; SBP_bac_5.

Pfam; PF00496; SBP_bac_5; 1.

PROSITE; PS01040; SBP_BACTERIAL 5; 1.

ERQUENCE SO BAA; 55661 MW; @4E7579A526CA74E CRC64;
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Last annotation update)
                                                                                                                     Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                        8.8%; Score 91.5; Di
27.6%; Pred. No. 29;
tive 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVP-----NTYYWRQGEDGKALPY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                     Ochrobactrum anthropi SV3.";
Eur. J. Biochem. 267:2028-2035(2000)
                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-JUN-2003 (TrEMBLrel. 24, Last ann
                                                                                                                                              Dipeptide transporter DppA homolog.
                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Serotype III;
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                      1018 LYQA-VAMLFGSL 1029
  183 FYEAKEGMLFDSL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 27.69
Matches 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus.
NCBI_TaxID=216495;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAMP factor.
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01-MAR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -----NAEQLKPYFKYLQIQIT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---NAEQLKPYFKYLQIQIT 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 SGYETNSTALGN----FSETKAVISLDNPSAVI-----VLDKEDIAVLYPDKTGYT 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
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                                                                                                                                                                                                                                                                                                                                     5 TLAIAGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVES-HLGSITPAAGAQ
                                                                                                                                                                                                                                                                                                                                                                       44; Gaps
                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete genome sequence and comparative genomic analysis of an emerging human pathogen, serotype V Streptococcus agalactiae."; Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396 (2002).
                                                                                                                                                                                                                                                                                44;
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                                                                                                                                                                                                               8.7%; Score 91; DB 16; Length 255; 24.5%; Pred. No. 12; tive 31; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Streptococcus agalactiae (serotype V).
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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                                                                                                                                                          255 AA; 28374 MW; 266DBB9D0B73562C CRC64;
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01-WAR-2003 (TrEMBLrel. 23, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   154 NTSIWVPGEPDKIIVYNE--TKPVAILNFKAF 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182 RATIYTKSKLDKEI-WNTRFTRDKKVLNVKEF 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          64 GSD---DIGYAIVWIKDQVNDVKLKVTLR---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=2603 V/R / Serotype V;
MEDLINE=22222988; PubMed=12200547;
invasive neonatal disease.";
Mol. Microbiol. 45:1499-1513(2002).
EMBL; AL766855; CAD47659.1; --
                                                                                                                                                                                                                                                 Similarity 24.59 S2; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                   SagaList; gbs2000; -.
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Best Local Similarity
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SEQUENCE 255 AA
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                                                                                                                                  Complete proteome
SEQUENCE 255 AA
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SDDIGYAI -- VWIKDQVNDVKLKVTLRNA------EQLKPYFKYLQIQITSGYET 111
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107 SGYETNSTALGN----FSETKAVISLDNPSAVI------VLDKEDIAVLYPDKTGYT 153
                       64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-99310339; PubMed=10382966;
Kawarabayasi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
Jin-no K., Takahashi M., Sekine M., Baba S.I., Ankai A., Kosugi H.,
Jin-no K., Takahashi M., Sekine M., Makazawa H.,
Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,
Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
"Complete genome sequence of an aerobic hyper-thermophilic
crenarchaeon, Aeropyrum pernix Kl.";
DNA Res. 6:88-101(1999).
BMBL, AP000061; BAA80205-1; -.
PIR; G72593; G72593.
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8.7%; Score 91; DB 17; Length 533;
Best Local Similarity 22.4%; Pred. No. 34;
Matches 49; Conservative 24; Mismatches 76; Indels '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP, P04268; IIC2.

GO: GO:0005840; C:intracellular; IEA.

GO: GO:0005840; C:intbosome; IEA.

GO: GO:0003735; F:structural constituent of ribosome; IEA.

GO: GO:0007155; F:structural constituent of ribosome; IEA.

GO: GO:0007155; F:structural constituent of ribosome; IEA.

GO: GO:0007155; F:structural constituent of ribosome; IEA.

GO: GO:0007155; F:structural constituent of ribosome; IEA.

GO: GO:0007155; F:structural constituent of ribosome; IEA.

InterPro: IPR001865; Ribosomal S2.

InterPro: IPR001865; Ribosomal S2.

InterPro: IPR001865; Ribosomal S2.

InterPro: IPR001863; Tropomyosin.
                                                                                                                                                                                                                                                                                                                                                                             Archãea, Crenarchaeota, Thermoprotei, Desulfurococcales, Desulfurococcaceae, Aeropyrum.
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Hypothetical protein; Complete proteome.
SEQUENCE 533 AA; 56481 MW; E8B53D791C353E31 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      150 TGYTNTSIWVPGEPDKI----IVYNETKPVAILNFKAFY 184
                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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                                                                             154 NTSIWVPGEPDKIIVYNE--TKPVAILNFKAF 183
                                                                                                                   182 RATIYTKSKLDKEI-WNTRFTRDKKVLNVKEF 212
                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, Created)
                                                                                                                                                                                                                      PRT;
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Pfam; PF00435; spectrin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00194; TROPOMYOSIN. SMART; SMO0150; SPEC; 1.
                                                                                                                                                                                                                                                                                                                    Hypothetical protein APE1216
                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                 01-NOV-1999 (TremBLrel.
                                                                                                                                                                                                                                                                                                   (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=56636;
                                                                                                                                                                                                                                                                                                                                                                Aeropyrum pernix.
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1376 KFTTVEVGSTVRQFTATDL----TPESAYIFRTSAKTRQGWGBPLEATVITTEKRERPA 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90 NAEQLKPYFKY-LQIQITSGYETNSTALGNFS-ETKAVISLDN-----PSAVIVLDKEDI 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 ------DVESHLGSITPAAGAQGSDDIGYAIVWIKDQVN------DVKLKVTLR 89
                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL, AF537107; AAN15075.1; -.
GO; GO:0016020; C:membrane; IEA.
GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66; Gaps
                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=22217368; PubMed=12230981; MEDLINE=22217368; PubMed=12230981; Yamagata M., Weiner J.A., Sanes J.R.; "SideAkicke: synaptic adhesion molecules that promote lamina-specific connectivity in the retina."; Cell 110:649-660(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.7%; Score 91; DB 13; Length 21 21.6%; Pred. No. 2.5e+02; Live 34; Mismatches 74; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00060; FN3; 13.
SMART; SM00409; IG; 7.
SMART; SM00408; IG=2; 6.
PROSITE; PS0835; IG LIKE; 5.
SEQUENCE 2169 AA; 2339477 MW; 06BFD900AEF19BD7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1540 -----TPHTISSVLVOWOPPKA----ESLNGLLGYRIYY 1570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 AVLYPDKTGYTNTSIWVPGEPDKIIVYNBTKPVAILNFKAFY 184
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Hypothetical protein PA2464.
: | : | | | : | | | : | | 1.59 SGRAVASFTVPPLPSGVHTVELVYT---PPLWLRFQSIY 204
                                                                                                                                            01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001282; Cytok receptor 2.
InterPro; IPR003962; FnII subd.
InterPro; IPR003961; FN III.
InterPro; IPR003991; FN III.
InterPro; IPR003599; IG.
InterPro; IPR003599; IG.
InterPro; IPR007110; Ig-like.
InterPro; IPR007189; Ig.
InterPro; IPR0031898; Ig.
Pfam; PF00041; fn3; 6.
Pfam; PF00041; fn3; 6.
PRNNTS; PF00041; ig, 6.
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les 48; Conservative
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                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                    Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                    Sidekick-1
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Q91118
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                                                                       RESULT 9
Q8AV58
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 AGIIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDV-ESHLGSIT-----PA 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARIAALGLLLPLAAGSAVAAEEGSSVKDAAKA-AVSSAIETGKNLLGGVSEGITSGRQSA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Schulsel J., Brandt P., Fartmann B., Holland R., Schulte U., Asign V., Hoheisel J., Brandt G., Fartmann G., Mewes H.W., Mannhaupt G., Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                     SEQUENCE FROM N.A.

SERAINS=ATCC 15692 / PAO1;

MEDLINB=20437337; PubMed=10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,

Garber R.L., Goltry L., Tolentino E., Westbrock-Waddman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

"Complete genome sequence of Pseudomonas aeruginosa PAO1, an

opportunistic pathogen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 TVRLINLTQTGALLVIDNDGYSNALVALANPDDVTV--PAKAGIRQTFVFEGG 157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 German Neurospora genome project;

R German Neurospora genome project;

R Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AL513444; CAC26681.1;

R GO; GO:0005524; F:ATP binding; IEA.

R GO; GO:0004553; F:hydrolase activity; IEA.

R GO; GO:0004672; F:protein kinase activity; IEA.

R GO; GO:0006472; F:protein kinase activity; IEA.

R GO; GO:0005072; P:protein amino acid phosphorylation; IEA.

R InterPro; IPR0017761; Glyco-hydro_33c.

R InterPro; IPR001764; Glyco-hydro_33c.

R InterPro; IPR001764; Glyco-hydro_31.

R Pfam; PF01915; Glyco-hydro_31.

R Pfam; PF01915; Glyco-hydro_31.

R Pfam; PF01915; Glyco-hydro_31.

R PRINTS; PR00133; GLHYDRLASE3.
                Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 90; DB 16; Length 174; Pred. No. 8.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63; Indels
                                                                                                                                                                                                                                                                                                                              EMBL, AE004674; AAG5852.1; -.
PIR; B83337; B83337.
Hypothetical protein; Complete proteome.
SEQUENCE 174 AA; 17626 MW; A00DDFCS25FCCE2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Probable beta-glucosidase 1.
                                                                                                                                                                                                                                                                                                                                                                                                               8.6%; Scor. No. 6...
26.0%; Pred. No. 6...
... 27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
                                      Pseudomonadaceae; Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                              Nature 406:959-964(2000)
    Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Neurospora crassa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5141;
                                                          NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 116
                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09C2C4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 ISLDNPSAVIVLDKEDIAVLYP--DKTG--YTNTSIWVPGEPDKIIVYNETKPV----- 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        113 GILNFSKAYVSLDDYRTAAAP----EOTGTVAVVKFKVLKEETSSISFEDTTSVPNAIDG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | :|:|| : : : : : | ::|:| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| | :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|| :|:|
                                                                                                                                                                                                                                                                                                                                                                                                                                 58 PAAGAQGSDDIGYAIVWIKDQVNDVKLKVTLRNA----EQLKPYFKYLQIQITSGYETNS 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 TALGNFSETKAVISLDNPSAVIVLDKEDIAV-----LYPDKTGYTNTS----IWVPG 161
                                                                                                                                                                                                                                                                                        22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu O., Gao W., Ding S.Y., Kenig R., Shoham Y., Bayer E.A., Lamed R.; "The Cellulosome System of Acetivibrio cellulolyticus Includes a Novel Type of Adaptor Protein and a Cell Surface Anchoring Protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GIIASAAALALLAGFATTQSPLNSFYATGTAQAVS-EPIDVESHLGSITPAAGAQGSDDI
                                                                                                                                                                                                                                                                                                                                                           709 AGFSKVWRYIYSWLSKSDADKAYAVGTSSS-----SKSGSQTYPYPEGYSSVQKPGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169 TVLFDWNGDRIQSGYSVIQPAVINLDMIKASY-----ITMGYDKNAAEVGEIIKATVKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Acetivibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36;
                                                                                                                                                DB 3; Length 896;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2; Length 942;
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ative 29; Mismatches 101; Indels
                                                                                                                                                                                                                  56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100358 MW; CABB5A638B352CA9 CRC64;
PROSITE; PS00775; GLYCOSYL HYDROL F3; 1.
PROSITE; PS00107; PROTEIN KINASE ĀTP; 1.
SEQUENCE 896 AA; 96788 WW; A89848BSDAE8D76B CRC64;
                                                                                                                                                                                                                                                                                    22 AGEA-----TTOSPLNSFYATGTAQAVSEPIDVESHLGSIT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 ---AILNFKAFYEAKEGMLFDSLP-----VIFNFQVLQ 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               280 ISEGILNLSRSYTALEVYRASESPEETGTLAVVGFKVLQ 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                  33; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.6%; Score 90; DB 4.2%; Pred. No. 93;
                                                                                                                                            8.6%; Score 90; DB 21.6%; Pred. No. 87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cellulosomal scaffoldin adaptor protein B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          942
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01-0CT-2003 (TrEMBLrel. 25, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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EMBL; AY221112; AAP48995.1; -.
SEQUENCE 942 AA; 100358 MW; CAE
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Best Local Similarity 24.2%
Matches 53; Conservative
                                                                                                                                                                                                                      40; Conservative
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                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=35830;
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Q9SOW9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 LTSAAKGIPATLQGSIEASLNGTSVTADVADVAKDVTLTDGKGVAVXSYDKNTLTNKLSD 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 IQITSGYETNSTALGNFSETKA----VISLDNPSAVIV----LDKEDIAVLYPDKTGYTN 154
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Saito Y., Hamanaka Y., Takizawa S., Benno Y.;
Saito Y.; Hamanaka Y., Takizawa S., Benno Y.;
"Rapid Detection of Lactobacillus helveticus in Fecal Samples of
Healthy Subjects Administered L. helveticus Yogurt using S-layer Gene-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45; Gaps
                                                                                                                                                                                                                                                                                            Yamamoto N., Shinoda T., Takano T.;
Yamamoto N., Shinoda T., Takano T.;
Yamamoto N., Shinoda T., Takano T.;
Yamamoto N., Submit and Sequence analysis of a gene encoding an extracellular proteinase from Lactobacillus helveticus CP790.";
Submitted (MAY-1999) cothe EMBL/GenBank/DDBJ databases.
EMBL, AB026985; BAA86287.1;
PIR, JC7306, JC7306, JC7306, JC7306, JC7306, GO:0009274; C:cell wall (sensu Bacteria); IEA.
GO: GO:0009199; F:structural constituent of cell wall; IEA.
InterPro; IPR004903; SLAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8.6%; Score 89.5; DB 2; Length 449;
24.0%; Pred. No. 36;
tive 33; Mismatches 87; Indels 45
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EMBL, AB061775; BAB72065.1; -.

EMBL, AC7306; JC7306.

GO, GO:0009274; C:Cell wall (sensu Bacteria); IEA.

GO, GO:0030115; C:S-layer; IEA.

GO; GO:0005199; F:structural constituent of cell wall; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
                                                                                                                         Lactobacillus helveticus.
Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11 IIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449 AA; 47798 MW; 8F2A22A2E5077326 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186 GLKFV---ISKVKAYDSANTNAV----SFYDAKSGLV 215
                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 TSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF03217; SLAP; 1.
PRINTS; PR01729; SURFACELAYER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-OCT-2003 (TrEMBLrel. 25,
  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 24.0% ses 52; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT.
Lactobacillus helveticus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Targeted Primers."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=1587;
                                                                                                                                                                                                 NCBI_TaxID=1587;
                                                                                                                                                                                                                                                                         STRAIN=CP790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Proteinase.
                                                                             Proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OR NEW SON THE SON TO SON THE SON TO SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE SON THE S
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                                                                                                                                                                                                                                                                                                                                                                                           60 -----AGAQGSDDIGYALVWIKDQVNDVKLKVTLRNAEQLKPYF------KYLQ 102
                                                                                                                                                                                                                                                                                                                                                                                                                            68 LISAAKGIPATLQGSIBASLNGTSVTADVADVAKDVTLTDGKGVAVYSYDKNTLTNKLSD 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 VKAGDDÝTMTLSGVG-FSFGKANAGKTLTFKLPEGVTVEGANYNKDDHKVTL-DQYGNVS 185
                                                                                                                                                                                                                                                                           ----ITPA-- 59
                                                                                                                                                                                                                                                                                                                               8 VSAAAAALLAVAPVAATAMPVNAATTVTTSTTTNKPTVDLSGAGSVSESKDTVNVTPSFT 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005618; C:cell wall; IEA.
GO; GO:0005618; C:cell wall; IEA.
GO; GO:0004650; F:hydrolase activity, acting on glycosyl bonds; IEA.
GO; GO:0004650; F:hydrolase activity; IEA.
GO; GO:00004505; F:hydrolase activity; IEA.
InterPro; IPR000961; FN III.
InterPro; IPR0009657; FN III.
InterPro; IPR000119; S.H.
InterPro; IPR0001119; S.H.
PFam; PF00041; fin3; 2.
Pfam; PF0025; Glyco.hydro_28; 1.
Pfam; PF0025; Glyco.hydro_28; 1.
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                                                                                                                                                                                                                  45; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (POLYGALACTURONASES).
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
EMBL; US0951; AAB08040.1; -.
                                                                                                                                                      Query Match

8.6%; Score 89.5; DB 2; Length 450;
Best Local Similarity 24.0%; Pred. No. 36;
Matches 52; Conservative 33; Mismatches 87; Indels 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matuschek M., Sahm K., Bahl H.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
!- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1148 AA; 122642 MW; E95BD0F2529FA10E CRC64;
InterPro, IPR004903; SLAP.
Pfam; PR03217; SLAP; 1.
PRINTS; PR01729; SURFACELAYER.
PRINTS:
                                                                                                                                                                                                                                                                           11 IIASAAALALLAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thermoangerobacter thermosulfurogenes (Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             155 TSIWVPGEPDKIIVYNETKPVAILNFKAFYEAKEGML 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.5%; Score 88.5; DB 2; 9.1%; Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell wall; Glycosidase; Hydrolase; Signal.
SIGNAL 1 30 POTENTIAL.
CHAIN 31 1148 POLYGALACTURONASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GLKFV---ISKVKAYDSANTNAV----SFYDAKSGLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Pred. No. 1.6e 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT; 1148 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polygalacturonase precursor (EC 3.2.1.82).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SMO0060; FN3; 2.
PROSITE; PSO0502; POLYGALACTURONASE; 1.
PROSITE; PSO1072; SLH DOMAIN; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thermosulfurogenes).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; S72635; S72635.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=33950;
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	qq
182 AFYEAKEGMLFDSL 195	ογ
125 HSFVLTGLKPNTLYTIQVQSVDANKNTSTPVTITQSTAPSTPSENIINVE 174	QQ
122 TKAVISLDNPSAVIVLDKEDIAVLYPDKTGYTNTSIWVPGEPDKIIVYNETKPVALLNFK 181	δλ
'IKQFYDNNVGDLKI	ФД
79 VNDV-KLKVTLRNAEQLKPYFKYLQIQITSGYETNSTALGNFSE 121	δλ
1 1	Dp
20 ILAGFATTQSPLNSFYATGTAQAVSEPIDVESHLGSITPAAGAQGSDDIGYAIVWIK-DQ 78	ΟŻ

Search completed: April 6, 2004, 12:41:16 Job time: 47 secs